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GenCore version 4.5
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OM protein - protein search, using sw model

March 1, 2001, 09:13:22 ; Search time 70.93 Seconds Run on:

(without alignments)
111.842 Million cell updates/sec

US-09-389-782A-1 1263 1 EPKSCDKTHTCPPCPAPELL......MHEALHNHYTQKSLSLSPGK 232 Perfect score:

Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

268485 seqs, 34193795 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:* /SID51/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SID51/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SID51/gcgdata/geneseq/geneseqp/AA2000.DAT:* /SIDS1/gcgdata/geneseg/genesegp/AA1993.DAT: /SIDS1/gcgdata/geneseg/genesegp/AA1994.DAT: /SIDS1/gcgdata/geneseg/genesegp/AA1995.DAT /SIDS1/gcgdata/geneseg/genesegp/AA1996.DAT /SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT /SIDS1/gcgdata/geneseq/geneseqp/AA1991../SIDS1/gcgdata/geneseq/geneseqp/AA1992.. /SIDS1/gcgdata/geneseq/geneseqp/AA1997 A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human IgG1 hinge/F	Protein from pCd51	Human immunoqîobul	Human kappa immuno	Sequence of the li	Linkered human IqG	Antiqenic peptide	Recombinant human	Recombinant human	Aggrecanase artifi	Aggrecanase artifi	Porcine CTLA-4-Ig
	GI	W26232	Y24154	R91806	R43685	P91918	P93558	W60037	W83962	W49073	W18574	W18575	Y15123
		18	20	17	14	10	10	19	19	13	18	18	21
	Query Watch Length DB	232	259	329	351	371	371	376	379	379	396	396	400
dР	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263	1263
	Result No.	1	7	æ	4	S	9	7	œ	6	10	11	12

Human soluble kit Human soluble kit Sequence of one ch Alpha-1-acid glyco IgG1 polypeptide.	Bovine LOX-1 extra Humanised 1D10 ant Human 1961, chain C Completely, humanis Amino acid sequenc	Heavy chaib sequen Human antitHBs hea Human NRBalpha/IgG Anti-HIV-11 recombi Reshaped CA4 antib	C 4 an C MPAT RI -FC ai of al anti	чиродн	
	Y24153 W05829 Y31669 R43339 W49816				W88464 W90207 W63763 W90206 R24442 R26531
4410701	010 - 00	20017	467 13 470 13 471 21 475 13 475 17 475 18		0 V 8 O H 4
1000.0	100.0 100.0 100.0	100.0 100.0 100.0 100.0	100.0 100.0 100.0 100.0		100.0 100.0 100.0 100.0
1263 1263 1263 1263	1263 1263 1263 1263	1263 1263 1263 1263 1263	1263 1263 1263 1263 1263	1263 1263 1263 1263 1263	1263 1263 1263 1263 1263
13 14 15 17	18 20 21 22	23 25 27	28 30 31 33 33	, , , , , , , , , , , , , , , , , , ,	40 41 44 44 5

ALIGNMENTS

RESULT

W26232 standard; Protein; 232 AA. Human IgG1 hinge/Fc region. 16-MAR-1998 (first entry)

Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; 1961; immunoglobulin; hinge region; Fc.

WO9728272-A1. Homo sapiens

97WO-US01470. 31-JAN-1997; 07-AUG-1997.

96US-0595043. (TECH-) TECHNOLOGENE INC. 31-JAN-1996; Sgarlato GD;

WPI; 1997-402624/37. N-PSDB; T80158.

Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins

Example 3; Page 133-134; 194pp; English.

Fusion

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         A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to C-terminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/Fc region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention at use useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein from pCd51neg1 comprising human IgG1 Fc region genomic DNA
                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                       DB 18; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSFGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia; low density lipoprotein; receptor; detection; immunoglobulin;
                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1263; DB 18; Length Best Local Similarity 100.0%; Pred. No. 1e-93; Matches 232; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y24154 standard; Protein; 259 AA
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97JP-0364981.
98JP-0349648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kakutani M, Masaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-418906/35.
N-PSDB; X88533.
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Synthetic.
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09-DEC-1998;
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and
                                                                       The present invention describes a fusion peptide which consists of the extracellular domain of a mammalian oxidized LDL (low density lipoprotein) receptor, fused to a partial heavy chain of a mammalian immunoglobulin containing all or part of the constant region. Oxidized LDL is a denatured form of LDL occurring in patients having rarteriosclerosis or hyperlipidaemia, and the fusion peptide can be used for the assay of oxidized LDL in biological samples from such patients, for the diagnosis of the disorders. It can also be used therapeutically for the prevention and treatment of arteriosclerosis any hyperlipidaemia. The present sequence represents the protein from the vector DNA of pcd5lnegl comprising human 1gG1 Ec region genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    28 epkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alkaline phosphatase; label; antibody; IgG; H-chain; C-region; CH1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunoglobulin gamma heavy chain constant region sequences.
             peptide for assay of oxidized LDL and for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant alkaline phosphatase (AP)-antibody fusion protein -
comprises AP fused downstream of antibody heavy or light chain,
useful as immunoassay reagent
                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                       Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hinge; fusion protein; chimera; immunoassay.
                                                                                                                                                                                                                                                                                                                     ; Score 1263; DB 20;
; Pred. No. 1.2e-93;
0; Mismatches 0;
                                         Example 1; Page 92-96; 105pp; Japanese.
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                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                   Matches 232; Conservative
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N-PSDB; T27385.
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Best Local Similarity
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                                                                                                                                                                                                                                                                         259 AA;
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14-MAY-1990
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                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                       121 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                        277
                 The gene coding for human alkaline phosphatase is fused downstream of a gene coding for either the variable and CHI regions of an antibody heavy chain or an antibody light chain. Coexpression of the H- and L-chain sequences, one of which is fused to the AP gene, results in production of AP-labelled antibodies suitable for use in immunoassays. The present sequence is from a human IgG heavy chain
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                              1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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0
                                                                                                                               Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acute lung injury; ischaemia reperfusion injury; inflammation
                                                                                                                                                                                                                                                                                           PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        kappa immunoglobulin light chain constant domain.
                                                                                                                             DB 17;
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0
                                                                                                                           100.0%; Score 1263; DB 17
100.0%; Pred. No. 1.6e-93;
ive 0; Mismatches 0;
Example 1; Page 13-15; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140.
/note= "Hing.
135.244
--- "CH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CH3 domain"
                                                                                                                                                                                                                                                                                                                                                             R43685 standard; Protein; 351 AA
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120..134
                                                                                                                                      Best Local Similarity 100.
Matches 232; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CYTE-) CYTEL CORP.
                                                                                                329 AA;
                                                                             constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                Sequence
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The sequences given in R43685-86 represent human immunoglobulin constant regions which were used in the production of the humanised p-selectin blocking antibody, along with the heavy and light chain variable region coding sequences of the murine monoclonal antibody PB1.3, given in R43687-88. The CDRs from PB1.3 heavy and light chains were substituted for the CDRs of human heavy and light chains. The humanised variable regions were inserted into expression vectors. By coexpression of appropriate combinations of heavy and light chains, several humanised antibodies can be expressed. Coexpression of pHCMV-17478RHa-sammalci-dhfr and pHCMV-1748RLa-KR-neo gives rise to the PB1.3/Humanised version A. Coexpression of pHCMV-1747-CL-KR-neo gives rise to the PB1.3 JHumanised antibodies selectively bind epitopes on P-selectin and class and chain and class and chain and class and other pathological coditions involving P-selectin and antibodies to it, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179
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                                                                                                                                       Anti-P-selectin antibody for ischaemia acute lung injury treatment useful to treat inflammation and pathological conditions of intercellular adhesion by competitive inhibition assays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of the linkered immunoglobulin gamma chain fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acute lung injury and ischaemia reperfusion injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1263; DB 14
Pred. No. 1.7e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
Polley MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 42..43
/note= "Insert site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Insert site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P91918 standard; protein; 371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
Paulson JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
nes 232; Conservative
                                                                                                                                                                                                                                                            82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 144..145
                                                   WPI; 1993-368423/46.
                                                                                                                                                                                                                                                            Example 10; Fig 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 AA;
                                                                                    N-PSDB; Q51547
Chestnut RW,
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Capon

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61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fas ligand; Fas antagonist; apoptosis related disease; liver diseas heart failure; kidney failure; graft-versus-host disease; antibody; myocardial infarction; ischemic restenosis; endotoxic shock.
                                                                                                                                                                               It is employed in the prepn. of CD4 fusions. CD4 fusion proteins have antiviral and immunomodulatory activity and are esp. useful treating HIV infections, regardless of genetic variation within the virus. They and antibodies raised against them can also be used diagnostically for assaying adhesons and their ligands.
                                                                                                                                                                                                                                                                                                                                                                                 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                        CD4, variants fused to other
                                                                                                                                                                                                                                                                                                                     Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "hFas antigen signal peptide" 30..376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic peptide hFas (nd29) containing Fc region.
                                                                                      New nucleic acid sequences encoding adheson, esp. partic. with trans-membrane domain inactivated or peptide, useful esp. for treating HIV infections
                                                                                                                                                                                                                                                                                                                   100.0%; Score 1263; DB 10; 100.0%; Pred. No. 1.8e-93;
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "hFas (nd29) protein"
                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                  Fig 4A-4B2; pp. 10/13-12/13; 78pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W60037 standard; Protein; 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0262521.
96JP-0290459.
96JP-0351718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-JP03978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                   Conservative
              Gregory TJ;
                                         WPI; 1989-114397/15.
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                         371 AA;
                                                          N-PSDB; N90736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1998
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9818487-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-1996;
27-DEC-1996;
              Capon DJ,
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W60037;
                                                                                                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
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                                                                                                                                                                                                                                                                                                                  It may be fused to the first 180 N-terminal residues of CD4 at the C-terminus. The fusion protein may be used for antiviral of immunomodulatory therapy particularly in treatment of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IgG1; gamma 1; immunoglobulin; CD4; fusion protein.
                                                                                                                                                                                                                        - useful in therapy and diagnostics, eg CD4 variants which are therapeutically useful for treating human immuno-deficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1263; DB 10;
11arity 100.0%; Pred. No. 1.8e-93;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human IgG1 (gamma 1) chain fragment.
                                                                       88US-0250785, US-104329
                                                                                                                                                                                                             Compsns. contg. abdesion variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P93558 standard; protein; 371
                                         88EP-0309194
                                                                                                                                                                                                                                                                                       Fig 4a-4b; ; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88WO-US03414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0104329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1990 (first entry)
                                                                                                                                    Gregory TJ;
                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                 WPI; 1989-131855/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                              371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH
                                                                                                                                                                               N-PSDB; N90779.
                                         03-OCT-1988;
                                                                       28-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO8902922-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 232;
           03-MAY-1989
                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                 infection
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This represents a recombinant metFc-OB protein which consists of an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity) protein. The invention provides a human OB protein suspension that contains at least 0.5 mg/ml of the human OB protein derivatised by attachment of the Fc region of an Ig to the N-terminus of OB, and has a pH 6-8. The suspensions are used to reduce weight, adiposity and blood lipid levels, to treat or prevent diabetes type II, and to increase lean mass and insulin sensitivity. They may be used in conjunction with insulin, hypoglyacemics, antihypertensives, diuretics, appetite suppressants etc. These suspensions are stable and active at physiological pH and are ready-for-use formulations that do not require freezing or freeze dryling. As they are very concentrated, only small volumes are required and they provide a sustained release effect, with increased potency and reduced frequency of injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWYVDGVEVHNAKTKPREEOYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ISKAKGΩPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 1β
                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin fragment - stable at physiological pH, used for e.g. reduction of weight and blood lipid levels, and for treatment of type II diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 epkscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Concentrated suspension of fusion of obesity protein with Fc
                 "can be optionally replaced with Glu"
                                                                                                         "can be optionally replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1263; DB 19. 100.0%; Pred. No. 1.8e-93; ive 0; Mismatches 0;
                                              "can be optionally
                                                                          "can be optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 5A-C; 47pp; English.
                                                                                                                                                                                                                                                                                                           Speed MA;
                                                                                                                                                                                                  98WO-US07828
                                                                                                                                                                                                                                               97US-0843971
                                                                                                                                                                                                                                98US-0059467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                              /note=
105
                 'note=
                                                                            /note=
107
                                                                                                         /note=
                                                                                                                                                                                                                                                                                                           French DL,
                                                                                                                                                                                                                                                                                                                                        1998-594525/50
 Misc-difference 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 232; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 AA;
                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                            Misc-difference
                               Misc-difference
                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V69685
                                                                                                                                                                                                                               14-APR-1998;
17-APR-1997;
                                                                                                                                       WO9846257-A1
                                                                                                                                                                                                  16-APR-1998;
                                                                                                                                                                     22-0CT-1998
                                                                                                                                                                                                                                                                                                           Brems DN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
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W49073
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                                                                                                                                                                                                                        This represents the antigenic peptide hFas (nd29) containing the FC region. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart failure, ischemic heart disease, acute kidney failure, graft-versus-host disease, ischemic restenosis of the heart, liver or kidney, and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant, metFc-OB protein; Fc region; immunoglobulin; Ig; OB; obssity; human; adiposity; blood lipid; diabetes type II; insulin; hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note≈ "can be optionally replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1263;
100.0%; Pred. No. 1.8
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant human metFc-OB protein.
                                                                                                                                                                                               Examples; Fig 5-9; 86pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
            MOCHIDA PHARM CO LTD.
OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W83962 standard; Protein; 379
                                                           Suda T, Yatomi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232; Conservative
                                                                                       WPI; 1998-271925/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference
                                                                                                       N-PSDB; V34430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-1999
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                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
            (MOCH ) N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W83962;
                                                            Nagata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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Gaps 9 9

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An artificial recombinant substrate, rAGG-1 (W18574), for aggreganase comprises the CD5 signal sequence, a FLAG epitope for MI monoclonal antibody detection, the intervallobular domain of human aggrecan, and human IgG1 hinge, CH2 and CH3 regions. It is the expression product of a DNA molecule (T69892) that can be incorporated into a vector for use in rAGG-1 prodn. in host cells. rAGG-1 can be used in cell culture systems to study the activity of aggrecanase, to detect new enzymatic cleavage sites, for the affinity purification of aggrecanase, to isolate aggrecanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding DNA, useful for studying aggrecanase activity e.g. by detection of cleavage products for monitoring onset or progression of osteoarthritis
                                                                                                                                                                                                                                     recombinant substrate; rAGG1; aggrecanase; aggrecan;
33..160
/label= Aggrecan
/note= "human aggrecan interglobular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant substrate for aggrecanase in vitro testing
                                                                                                                                                                                                    Aggrecanase artificial recombinant substrate rAGG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bartnik E, Buettner F, Caterson B, Eidenmueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Hinge
/note= "human IgG1 hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CH3
/note= "human IgGl CH3 region"
                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
/note= "CD5 signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "human IgG1 CH2
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 15-16; 28pp; English.
                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spacer
                                                                                                   W18574 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                       25..32
/label= FLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96EP-0100682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH2
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                      osteoarthritis; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                       Homo sapiens;
synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-365948/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T69892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-1996;
                                                                                                                                                                     17-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUL-1997
                                                                                                                                                                                                                                                                                      Chimaeric s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hughes C;
                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                    W18574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                   RESULT
                                                                                     W1857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a recombinant human MetFc-OB fusion protein. The invention provides Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its analogue is linked, either directly or indirectly using a linker, to the N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins are claimed to demonstrate increased stability and clearance rate and decreased degradation as compared to OB protein or a fusion of Fc to the C-terminus of the OB protein. These Fc-OB fusion proteins are also claimed to be useful for treating excess associated with excess fat such as diabetes, high blood lipid level, arterial sclerosis and stroke.
                                                                                                                                Recombinant human MetFc-OB protein; chimeric; immunoglobulin; diabetes; high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins of OB and Fc - used for treating e.g. excess weight, diabetes, arterial sclerosis, arterial plaque, high blood lipid level, gall stones or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1263; DB 19; Length 379; 100.0%; Pred. No. 1.8e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                 /note= "Recombinant human Fc-OB protein" 234..379
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                                                                                                                                                                                                                                                                                                    "Human OB protein"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                               Recombinant human MetFc-OB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 3A-3C; 107pp; English.
W49073 standard; Protein; 379 AA
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                                                                18-NOV-1998 (first entry)
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                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                     11-DEC-1997;
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(FARH ) HOECHST AG.
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                                                                                                                                                                                                                    osteoarthritis
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Homo sapiens.
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                                                    Bartnik E,
                                                                          Hughes C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Region
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Y15123
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                                                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                          121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                              285 iskakgqprepqvytlppsrdeltknqvsltclvkgfypsdlavewesngqpennykttp 344
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                   EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
cDNA by functional cloning, to screen for aggrecanase inhibitors, in methods for monitoring the onset or progression of osteoarthritis, and in diagnostic aids. Another rAGG-1 (W18575) has alanine at amino acid position 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Artificial recombinant substrate; rAGG1; aggrecanase; aggrecan;
                                                                                                                                             Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.160
/label= Aggrecan
/note= "human aggrecan interglobular domain"
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aggrecanase artificial recombinant substrate rAGG-1.
                                                                                                                                            DB 18;
                                                                                                                                          cch 100.0%; Score 1263; DB 18 18 Similarity 100.0%; Pred. No. 1.9e-93; 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "human IgG1 hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "human IgG1 CH3 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Sig_peptide
/note= "CD5 signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CH2
/note= "human IgG1 CH2
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/label= Spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W18575 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= FLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoarthritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimaeric Homo sapiens;
Chimaeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
25..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
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                                                                                                                                          Query Match
Best Local Similarity
Matches 232; Conserv
                                                                                     396 AA;
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                                                                                       Sequence.
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W18575
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Porcine CTLA-4; soluble protein; xenograft; organ transplant; B7; CD28; xenograft-specific immunosuppression; recipient T-cell; anergy; co-stimulatory signal 2; homology; human CTLA-4; bovine CTLA-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                An artificial recombinant substrate, rAGG-1 (W18575), for aggreganase comprises the CD5 signal sequence, a FLAG epitope for MI monoclonal antibody detection, the interglobular domain of human aggrecan, and human IgG1 hinge. CH2 and CH3 regions. It is the incorporated into a vector for use in rAGG-1 prodn. in host cells. AGG-1 can be used in cell culture systems to study the activity of aggrecanase, to detect new enzymatic cleavage sites, for the affinity purification of aggrecanase, to isolate aggrecanase cDNA by functional cloning, to screen for aggrecanase inhibitors, in methods for monitoring the onset or progression of osteoarthritis, and in diagnostic aids. Another rAGG-1 (W18574)
                                                                                                                                                                 Recombinant substrate for aggrecanase in vitro testing - and encoding DNA, useful for studying aggrecanase activity e.g. by detection of cleavage products for monitoring onset or progression
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  В;
  Eidenmueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 1263; DB 18 Best Local Similarity 100.0%; Pred. No. 1.9e-93; Matches 232; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   Claim 3; Refer to page 15-16; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          has glycine at amino acid position 34.
  m,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
162..168
Caterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y15123 standard; Protein; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine CTLA-4-Ig construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
  ᄄ
Buettner
                                                                                WPI; 1997-365948/34.
N-PSDB; T69893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Domain Domain

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(see also W14761) and a human 1961 heavy chain can be transiently expressed in COS cells transfected with a human KL-Ig CDNA construct (T63109) in vector CDNB, a corrected KL-Ig construct (W14765) has also been prepd. KL-Ig can also be produced as a dimer stabilised by intermolecular disulphide bonds or a peptide linker. The stabilised KL-Ig dimers have a more favorable cell prolliferation:mast cell activation ratio than native KL and can stimulate haematopoietic recovery or stem cell/progenitor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A fusion protein (W14764) between human soluble kit ligand (KL)
                                                                                                                                                                                                                                                                                                                                                                                                                  Covalent dimers of kit ligand or FLT-3/FLK-2 ligand increased activity in promoting cell proliferation
                                                                                    26..424
/label= Mat_protein
/note= "human KL-IgG fusion"
                                                                    "KL signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 43-44; 88pp; English.
                                            /label= Sig_peptide
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mobilisation with less toxicity.
                                                                                                                                                                                                                            95WO-US03866
                                                                                                                                                                                                                                                             94US-0220379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                      /note=
                                                                                                                                                                                                                                                                                                                               Nocka KH;
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-351198/45.
                                                                                                                                                                                                                                                                                             (CYTO-) CYTOMED INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 232; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 AA;
                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T63109
                                                                                                                                                        WO9526199-A1
                                                                                                                                                                                                                            28-MAR-1995;
                                                                                                                                                                                                                                                           28-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1997
                                                                                                                                                                                          05-OCT-1995.
                                                                                                                                                                                                                                                                                                                               Lobell RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                   Key
Peptide
                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
W14765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ōλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is porcine CTLA-4-Ig construct for xenograft specific immunosuppression. In a pig-to-human transplantation, the soluble protein could comprise the extracellular domain of porcine CTLA-4 fused to a human C gamma I chain of IgG1. This construct was subcloned into the expression vector pHOOK-3TM and used to transfect DAP.3 or CHO-K1 cells. pCTLA-4-Ig preferentially binds to porcine B7 and blocks its interaction with CD28 on recipient T-cells. This is useful as a species-specific reagent to inhibit human T-cell proliferative responses to a variety of stimulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                             Inhibiting T-cell mediated rejection of xenotransplanted organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1263; DB 21; Length 400;
Pred. No. 2e-93;
Mismatches 0; Indels 0;
/label= Flexible_linker
/note= "Denotes the junction between pCTLA-4"
169..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kit ligand; c-kit proto-oncogene; cytokine; growth factor; haematopoietic cell; cell proliferation; stem cell; anaemia; thrombocytopaenia; therapy; IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human soluble kit ligand-IgG fusion protein.
                                                                                                                                                                                                                                           (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
                                            /label= IgG1_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 4; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W14764 standard; Protein; 424
                                                                                                                                                                                                         98GB-0009280
                                                                                                                                                                        99WO-GB01350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                             Dorling A;
                                                                                                                                                                                                                                                                                                             WPI; 2000-038815/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 AA;
                                                                                                    409957266-A2
                                                                                                                                                                                                          30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                      11-NOV-11999
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Best Local Simi
Matches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kit ligand;
                                                                                                                                                                                                                                                                             Lechler IR,
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δŏ g RESULT W14764 Ношо

Matches

exhibit

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Gaps
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                                                                                                                                                                                       NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                   253 nwyvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiekt
                                                                                                                                                                                                                                                                                 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
    Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human soluble kit ligand-IgG fusion protein (corrected).
  DB 16;
100.0%; Score 1263; DB 16
100.0%; Pred. No. 2.1e-93;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W14765 standard; Protein; 424 AA
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chaim homodimer; expression vector; HIV; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector - for preventing and treating HIV infection useful as a diagnostic agent
                                                     one chain of a CD4-gamma 1 chimeric heavy chain
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                   Joca
1..204
/label= CD4
-+e= "1..25 =
                                                                                                                                                                                                                 205..219
/label= hinge
                                                                                                                                                                                                                                           220..329
/label= CH2
330..436
/label= CH3
                                                                                                                                                                                                                                                                                                                                                                                                                            (PROG-) PROGENICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                 91US-0654205
                                                                                                                                                                                                                                                                                                                                                                        92WO-US01152
                                                                                          CD4-gamma 1 chimeric heavy therapy; diagnostic agent;
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maddon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-299758/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 232; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q27830
                                                                                                                                                                                                                                                                                                                                                                      10-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1991;
                                                                                                                                                                                                                                                                                                                  WO9213559-A.
                          28-JAN-1993
                                                     Sequence of
                                                                                                                                                                                                                                                                                                                                           20-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beaudry GA,
                                                                    homodimer.
                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
R26530;
                                                                                                                                                                            Region
                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                               Region
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                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see also W14761) and a human igGl heavy chain can be transiently expressed in COS cells transfected with a human KL-1g cDNA construct (163110) in vector CDM8. KL-Ig can also be produced as dimer stabilised by internalceular disulphide bonds or a peptide linker. The stabilised KL-Ig dimers have a more favorable cell proliferation:mast cell activation ratio than native KL and can stimulate haematopoietic recovery or stem cell/progenitor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 iskakgqprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A fusion protein (W14765) between human soluble kit ligand (KL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                              - exhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kit ligand; c-kit proto-oncogene; cytokine; growth factor;
haematopoietic cell; cell proliferation; stem cell; anaemia;
thrombocytopaenia; therapy; 1961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Covalent dimers of kit ligand or FLT-3/FLK-2 ligand increased activity in promoting cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1263; DB 16;
100.0%; Pred. No. 2.1e-93;
ive 0; Mismatches 0;
                                                                                                        1..25
/label= Sig_peptide
/note="KL signal peptide"
26..424
/label= Mat_protein
/note= "human KL-IgG fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 46-48; 88pp; English.
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mobilisation with less toxicity
                                                                                                                                                                                                                                                          95WO-US03866
                                                                                                                                                                                                                                                                                     94US-0220379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232; Conservative
                                                                                                                                                                                                                                                                                                                                           Nocka KH;
                                                                                                                                                                                                                                                                                                                (CYTO-) CYTOMED INC.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-351198/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AA;
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T63110
                                                                                                                                                                                                                                                                                    28-MAR-1994;
                                                                 Homo sapiens
                                                                                                                                                                                                     WO9526199-A1
                                                                                                                                                                                                                                                         28-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                          Lobell RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                       Peptide
                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                               Human CD4 cDNA was excised from pSP6T4 and cloned into M13mp18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1263; DB 13
ilarity 100.0%; Pred. No. 2.2e-93;
Conservative 0; Mismatches 0;
Example; Fig 3; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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R26530 standard; Protein; 435 AA

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US-09-389-782A-2 2179 1 MNKWLCCALLVLLDIIEWTT......QKLFLEMIGNQVQSVKISCL 401 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

374700 seqs, 117207915 residues Searched:

374700 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_organelle:* sp_archea:* sp_bacteria:* sp_rodent:* sp_plant:* SPTREMBL_15:* sp_fung1:* sp_phage:* sp_mhc:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	008712 mus musculu	008727 rattus norv	000300 homo sapien	Q9uhp4 homo sapien	095407 homo sapien	Q9pus0 salvelinus	Q62327 mus musculu	088734 mus musculu	075509 homo sapien	Q16042 homo sapien	035305 mus musculu	Q9y6q6 homo sapien	Q85308 cowpox viru	O57098 camelpox vi	O57305 cowpox viru	O57284 camelpox vi	O57097 camelpox vi	057110 variola vir	O57111 variola vir
		TD	1 008712	1 008727	000300	Q9UHP4	095407	3 Q9PUS0	1 Q62327	1 088734	075509	016042	1 035305	09¥6Q6	2 Q85308	2 057098	2 057305	2 057284	2 057097	2 057110	2 057111
		datch Length DB	401 1	401	401 4	372 4	300 4	302 1	459 1	482 1	655 4	439 4	625 1	616 4	355 1	349 1	349 1	349 1	349 1	349 1	349 1
æ	Query	Match L	100.0	95.4	86.8	82.1	19.5	17.9	14.4	13.9	13.8	13.7	12.3	12.2	10.4	10.3	10.2	10.1	10.1	10.1	10.0
	C	score	2179	2079	1892	1789	424.5	390.5	314	302.5	301.5	298	268.5	266.5	226	224	222.5	221	220	219	218
	Result	NO.	1	7	æ	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19

'089118 variola vir	O57099 monkeypox v		\sim	Q85407 variola vir	057291 monkeypox v					O57116 cowpox viru	O57119 cowpox viru					O57115 cowpox viru	057123 cowpox viru		O57117 cowpox viru	073559 cowpox viru	O57122 cowpox viru	057121 cowpox viru	092956 homo sapien		O57091 ectromelia
089118	057099	860680	057112	085407	057291	057100	057101	057102	057118	057116	057119	057277	057103	057108	057120	057115	057123	057109	057117	073559	057122	057121	092956	Q9UM65	057091
12	12	12	12	12	12	13	12	12	12	12	13	12	12	12	12	12	12	12	12	12	12	12	4	4	12
349	349	349	348	348	349	349	349	349	360	350	347	348	348	348	326	347	350	349	351	351	326	351	283	283	320
10.0	10.0	6.6	6.6	9.9	6.6	6.6	6.6	6.6	8.6	9.6	9.6	9.7	9.7	9.7	9.7	9.7	9.6	9.6	9.5	9.5	9.4	9.4	9.4	4.6	9.4
218	217.5	216	215.5	215.5	215.5	215.5	215.5	215.5	214.5	214	212.5	212	212	212	211.5	210.5	209.5	209	207.5	207.5	205.5	204.5	204	204	204
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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008727
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008727
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SUBCELLULAR LOCATION: EXTRACELLULAR.
118SUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
BRAIN, HEART, KIDNEY, STOWACH, INTESTINE, SKIN, CALVARIA AND
PLACENTA. NOT DETECTED IN SPLEEN.
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
15 TO DAY 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNAT 180
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BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
SMISSI.
                                                                                             SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2179; DB 11; Length 401; 100.0%; Pred. No. 6.7e-164; ive 0; Mismatches 0; Indels 0;
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1143
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                                                                                                                                                                                                                   MGD; MGI:109587; Opg.
INTERPRO; IPR000488;
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Matches 401;
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RECTISSUE INTESTINE;

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181 HDNVCSGNREATOKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVERI
                                                                                                      HININ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-2000 (TrEMBLRel. 15, Last annotation update)
01-CCT-2000 (TrEMBLREL) 15, Last annotation update)
0STEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
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BY SIMILARITY.

OI OSTEOPROFEGERIN.

A X TNRR-CYS.

G TNRR-CYS 2.

TNRR-CYS 2.

TNRR-CYS 3.

TNRR-CYS 3.
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"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OSTBOPROTEGERIN PRECURSOR (OSTBOCLASTOGENESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
HORROSILE DR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                Length 401;
                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                            FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
                                                                                                                                                                                                                                Score 2079; DB 11;
Pred. No. 5e-156;
                                           SIMILARITY.
  SIMILARITY
                                                                                                                                                                                                                                                                              10; Mismatches
BY SIMILARI
BY SIMILARI
BY SIMILARI
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                            46192 MW;
                                                                                                                                                                                                                                95.4%;
94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                              Conservative
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105
142
160
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TISSUE=LUNG FIBROBLAST;
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87
118
145
98
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                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                              Matches 379;
                   DISULFID
                                                                                         CARBOHYD
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DISULFID
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OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
                                                                                                                                                                                                                                                                                                                                     FISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED AN UNBER OF OTHER HEMAPOPOIETIC AND IMMUNE ORGANS. NOT DETECTED THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.

-! SIMILARITY: CONTAINS A LA-NGFR/THER-TYPE CYSTEINE-RICH REGION.

EMBL, AB002146; BAA25910.1;
           Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N. Sato Y., Goto M., Yamaquchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.; Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                 "Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor."; Eur. J. Biochem. 24:685-691(1998).
                                                                                                                                                                                                                                                                               STROMAL CELLS AND OSTEOCLAST PROGENITORS.
SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 401;
                                                                                                                                                                    Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.; "Cloning and characterization of the gene encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> D (IN REF. 2 AND 3).
EB42FA51C9D7C71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.8%; Score 1892; DB 4;
85.6%; Pred. No. 2.7e-141;
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; Mismatches
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SIMILARITY
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TWER-CYS 3.

TWER-CYS 4.

DEATH DOMAIN.

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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
                                                                                                                                                                                                                                                                                                           SIMILARITY).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
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AB008821; BAA32076.1; JOINED.
U94332; AAB53709.1; -.
                                                                                                                                        TISSUE=PLACENTA;
MEDLINE=98351569; PubMed=9688283;
MEDLINE=98151033; PubMed=9492069;
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SEQUENCE FROM N.A.
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Matches 344;
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SEQUENCE FROM N.A.
MEDLINE=99087326; PubMed=9872321;
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.L., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
"Genomic amplification of a decoy receptor for Fas ligand in lung and
 RDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALMESLPGKKISPEEIERTRKTCKS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V. Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                    241 KDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP
                                                                                        SEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPKTVTHSLRKTMRFLHSFTMYRLY
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99253915; PubMed=10318773;
Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 424.5; DB 4; Length 300; Pred. No. 7.1e-26;
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                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).

EMBL; AF104419; AAD03056.1; -.

EMBL; AF134240; AAD29688.1; -.

EMBL; AF217796; AAF35244.1; -.

EMBL; AF217799; AAF33685.1; -.

EMBL; AF217794; AAF33686.1; -.
                                                                                                                                                                                                                                                                   300 AA.
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                        DECOY RECEPTOR 3 (M68) (M68C) (M68E)
DCR3 OR TR6.
                                                                                                                                                                                                                                                                     PRT;
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39.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 396:699-703(1998).
                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best.Local Similarity
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                                                                                                                                                                361 QKLFLEMIGNOV
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                  TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
                                                                     KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                        THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER 239
                                                                                                                                                                                                              IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 299
                                                                                                                                                                                                                                                                                    ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK 359
                                                                                                                                                                                                                                                                                                    YCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTV 141
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
"Cloning and Expression of Osteoprotegerin from Homo sapiens.";
Sheng Wu Hua Haueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999)
EMBL: AFI34187; AAF201681;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      Score 1789; DB 4;
Pred. No. 3.2e-133;
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86.0%; Pred. No. 3.2e-
tive 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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--CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ 175
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"The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure and Characterization of the two Transcripts.";
EMBL: X14619; CAA74969.1; -.
EMBL: X14621; CAA74969.1; -.
EMBL: X14621; CAA74969.1; JOINED.
EMBL: X14621; CAA74969.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGSC 121
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                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                      STRAIN=NOD;
MEDLINE=59178848; PubMed=7873884;
POWell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
"Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                  S -> T.

T -> I.

F -> I.

S -> E.

Y -> C.

W; 6C5ID2CFIC4626DF CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 314; DB 11; 34.6%; Pred. No. 5.8e-17; Live 20; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                              INTERPRO; IPR001368; -.
PFAM; PF00020; TRFR_C6; 4..
PROSTIE; P850052; TNFR_MGFR_1;
PROSITE; P850050; TNFR_MGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            48686 MW;
                                                                                                                                                                                                                        Mamm. Genome 5:726-727(1994).
EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
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178 PGNASTDAVCA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGNATHDNVCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                    87
93
268
345
421
459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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SEQUENCE FROM N.A.
                                                                                                        [1]
SEQUENCE FROM N.A.
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                                                                                      NCBI_TaxID=10090;
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VARIANT
SEQUENCE
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Bobe J., Goetz F.W.;

A tumor necrosis factor receptor homolog is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";

Biol. Reprod. 0:0-0(1999).

EMBL; AR156738; AAD56428.1; -.

HSSP: P19438; IEXT.

INTERPRO; IPR001561; -.

INTERPRO; IPR001368; -.
                                                                                                                         VCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKC 145
                                                                                                                                                                                               34 PIYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPITCGPCPPRHYTQFWNYLERCRYCNV 93
   Gaps
                                  PKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 DRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-MCAENO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 PDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNV---CSGNREATQKCGIDVTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 DPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVKQECNRTHNRVCECEEGRYL - - EIEFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salvelinus fontinalis (Brook trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
NCBI_TaxID=8038;
88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                                                                                                                                                                      302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 3.46
34; Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.9%; Score 390.5; 42.7%; Pred. No. 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM: PF00020; TNFR.c6; 4.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                              212 ERAVIDEVAFODISIKRLORLLOAL 236
                                                                                                                                                                                                                                             203 EEAFFREAVPTKIIPNWLSVLVDSL 227
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AA; 34037 MW;
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062327;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15,
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches

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RESULT 962327 DA PE

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Gaps

Length 459;

us-09-389-782a-2.rspt

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Pred. No. 8.5e-16;
  29.0%;
                 91; Conservative
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                                                                                                                                                                                                                                                                               295 LLALMESLPGKKIS 308
                                                                                                                                                                                                                                                                                                     312 LLPSMEATGGEKSS
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    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Best Local Simi
Matches 62;
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Matches
                                                                                                                                     124
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"Identification and functional characterization of DR6, a novel death domain-containing TNF receptor.";
                                                                                                                                                                                                                                50 LKQHCT-----VRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHN 102
                                                                                                                                                                                                                                                     64 VKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQN 123
                                                                                                                                                                                                                                                                              RVCECEEGRYLEIEF-----CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETS 155
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                 ---QLLCDKCAPGTY 49
                                                                                                                                                                                               6 LWVALVFELQL - WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                     075509;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
THER-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (THER-RELATED DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                          35;
                                                                                                                                     DB 11; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini; Hominidae; Homo.
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF068868; AAC34583.1; -. EMBL; AL096801; CAB75692.1; -.
                                                                                                482 AA; 51106 MW; F6C15046B48FF83C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71844 MW; 48939391C4852A33 CRC64;
                                                                                                                                                         84;
                                                                                                                                 13.9%; Score 302.5; DB 33.2%; Pred. No. 5e-16; Live 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             655 AA
                                                                                                                                                                                 5 LCCALLVLLDIIEWTTQETLPPKYL--HYDPETGH--
                                                                                                                                                                                                                                                                                                                                         STDVCRPHRICS----ILAIPGNASTDAVCA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN_1
                                                                                                                                                                                                                                                                                                                             SKAPCIKHTNCSTFGLLLIQKGNATHDNVCS 186
EMBL; Y14623; CAA74969.1; JOINED. EMBL; Y14679; CAA74969.1; JOINED. HSSP; P19438; INCF.
INTERPRO; IPRO01368; -. PFAM; PF00020; INFR_C6; 4. PROSITE; PS00652; INFR_NGFR_1; 2. PROSITE; PS50050; INFR_NGFR_2; 3. PRODOM; PD000771; -; 1.
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INTERPRO; IPR001368; -,
PFAM; PF00020; TNFR_c6; -,
PROSITE; PS00652; TNFR_NGFR_1; UNKN
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50007; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                  Query Match 13.99
Best Local Similarity 33.23
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P07174; 1NGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR6 OR DJ181J13.1
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SEQUENCE
                                                                                                SEQUENCE
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Length 655;

DB 4;

Score 301.5;

13.8%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 RPKVLSSIQEGTVP-----DNTSSARGKEDVNKTLPNLQVVNHQQGPHRH----ILK 311
                                                                                                                                                                                                                                                                                                                                    CPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDN 183
                                                                                                                                                                                                                                                                                                                                                                                                                          184 VC----SGNREATQKCGIDVTLCEEAFFRFAVPTK-IIPNWLSVLVDSLPGTKVNAESVE 238
                                                                                                                                                                               64 PCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKRRHSSQEQTFQLLKLWKHQN----RDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI-----EFCLKHRSCPPGSGVVQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVAR 129
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      Gaps
                                                             10 LVLLDIIEWTTQE-----TLPPRYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 YDPETGH------QLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91370690; PubMed=1966549;
MEDLINE=91370690; PubMed=1966549;
MEDLINE=91370690; PubMed=1966549;
Brockler Z., Loesslauer H., Gubler U., Pan Y.C., Lahm H.W., Gentz R., Brocklaus M., Lesslauer W.;
"Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences.";
Cytokine Z.231-237(1990).
EMBL; 863368; AAB19824.1; --
HSSP; P25942; ICDF.
                                                                                                  |:|| : || : || : || 30 LILLGFLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 439;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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: 46090 MW; FEBCBE329CC67FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NoV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR.
40; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.7%; Score 298; DB 4; La
larity 35.6%; Pred. No. 1e-15;
Conservative 15; Mismatches 75;
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PFAM; PF00020; TNRR_OGS; 4.
PROSITE; PS00052; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
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190 ESDVVCSSSMTLRRPPKEAQAYLPSLIVLL--LFISVVVVAAIIFGVYYRKGGKALTANL

PRT;

PRELIMINARY;

180 THDNVCSGN-----REATQKCGIDVTLCEEAFFRFAVPTKII---

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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-2000 (TrEMBLrel. 12, Last annotation update)
RECEPTOR ACTIVATOR OF WIF-KAPPA-B PRECURSOR (TWF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                       217 PNWLSVLVDSLPGTKVNAESVERIKRRH---SSQEQTFQLLKLWKHQNRDQEMV 267
                                                                                                                                                                                                                                                                                    Q9Y6Q6
Q9Y6Q6;
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Q9Y6Q6
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                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-CTT-2000 (TrEMBLrel. 15, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                  MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINKED (GLCNAC. . .) (P. F8C1872E99511D8E CRC64;
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SIGNAL 1 30 POTENTIAL.
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                                     625 AA
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                    INDUCED CYTOKINE RECEPTOR) (RANK).
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                                    PRELIMINARY;
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625 AA;
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Matches 88; Conserv
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Galibert L.;
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RESULT 11
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-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-i- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEYELS I
- SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
                                                                          Galibert L.;
"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS A LA-NGFR/INFR-TYPE CYSTEINE-RICH REGION. EMBL; AF018253; AAB86809.1; - HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
RECEPTOR ACTIVATOR OF NF-KAPPA-B.
EXTRACELLULAR (POTENTIAL).
SEQUENCE FROM N.A.
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                         INTERPRO: IPR001368; -
PFAM; PF00020; TNFR_c6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
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THER-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CALLVLLDIIEWTTQETLPP--KYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%; Score 268.5; DB 11; Length 625; 29.9%; Pred. No. 3.2e-13; Live 34; Mismatches 123; Indels 49;
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SEQUENCE FROM N.A.
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NCBI_TaxID=28873;
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01-JUN-1998
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                                                                                                                                                                                                                                                                                                63 VPCPDHSYTDSWHTSDECVYCSPVC---KELQSVKQECNRTHNRVCECEEGRY--LEIEF 117
                                                                                                                                                                                                                                                                                                                                                                                     CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKG 177
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                             16 LICALLARLQV----ALQIAPPCTSEKHYE-HLGR--CCNKCEPGKYMSSKCTTTSDSVC
                                                                                                                                                                                                                                                                                                                                           LPCGPDEYLDSWNEEDKCL-LHKVCDTGKALVAVVAG-NSTTPRRCACTAGYHWSQDCEC
                                                                                                                                                                                                                                                                                                                                                                                                                      127 CRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFSSTDKCRPWTNCTFLGKRVEHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCCALLVLLDIIEWTTQETLPP - - KYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PNWLSVLVDSLPGTKVNAESVERIKRRHSS-------QEQTFQLLKLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 PDQGGVCQGTCVGGGPYAQGEDARML-SLVSKTEIEEDSFRQMPTEDEYMDRPSQPTDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALMESLPGKKISP---EEIE------RTRKT----CKSSEQLLKLLSLWRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 ANLWHWINEACGRLSGDK -- ESSGDSCVSTHTANFGQQGACEGVLLLTLEEKTFPEDMCY
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                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E3DE9A7A08196F81 CRC64;
                                                                                                                            12.2%; Score 266.5; DB 4; Length 616; 24.4%; Pred. No. 4.5e-13; ive 54; Mismatches 166; Indels 115;
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STRAIN=BRIGHTON RED;
MEDLINE=90177240; PubMed=2309453;
Parsons B.L., Pickup D.J.;
"Transcription of orthopoxvirus telomeres at late times during infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 NATHDNVCSGNREATQK------CGIDVTLCEEAFFRFAVPTKII---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1906 (TrEMBLrel. 15, Last annotation update)
SECRETED RECEPTOR BINDING TUMOR NECROSIS FACTOR (CRMB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRIGHTON RED;
MEDLINE-83117629; PubMed-6961398;
Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
"Sequence of terminal regions of compox virus DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982)
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BY SIMILARITY
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                                                              MM;
                                                              66033
                                                                                                                                                Best Local Similarity 24.49
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 175:69-80(1990).
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01-NOV-1996 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                         616 AA;
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NCBI_TaxID=10243;
                    CARBOHYD
CARBOHYD
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SEQUENCE FROM N.A.
STRAIN-BRIGHTON RED;
MEDLINE-94378510; Pubmed-8091665;
Hu F.O., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a secreted form of the type II TNF receptor.";
Virology 204:343-356(1994).
EMBL: L08906; AAA6052.1; -.
HSSP; P19438; LEXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 RKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI -- 115
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SEQUENCE FROM N.A.
STRAIN=BRIGHTON RED;
MEDLINE=91196263; PubMed=2014645;
Hu F.Q., Pickup D.J.;
"Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution.";
Virology 181:716-720(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Camelpox virus (strain CP-1).
Viruses; dspNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LLVLLDIIEWTTQETLPPKYLHYDPETG------HQLLCDKCAPGTYLKQHC--TVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLLLSCIIINSDITP-----HEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 ----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLIQKG-NATHDNVC----SGNREATQKCGIDVTL----CEEAFFRFAVPTKIIPNWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 VLVDSLPG-----TKV---NAESVERIKRRHSSQEQTFQLLKLWKHQNRDQEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 MPHSESVTLVGDCLSSVDIYILYSNTNTQDYETDTISYHVGNVLDVDSHMPGR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 V--KKIIODIDLCESSVORHLGHSNLTTE------OLLALMESLPGK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
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Loparev V. N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U87839; AAB94356.1; "
                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Last Sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 226; DB 12; 24.1%; Pred. No. 3.7e-10;
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Matches 85; Conservative
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                                                                                                                                                                                                                                 82 YCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI-----EFCLKHRSCPPGSGVVQAGT 135
                                                                                                                                                                                                                                                  253 CTLNFEIKCNNKGSSSKQ-----LTKAKNDDGIMPHS--ETVTLAGDCLSSVDIYILYS 304
                                                                                                                                                                                                                                                                                         136 PERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKG-NATHDNVC----SGNR 189
                                                                                                                                                                                                                                                                                                                   144 SAGDVICSPCGLGTYSRTVSSADKC-EPVPSNTFNYIDVEINLYPVNDTSCTRTTTTGIS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LLVLLDIIEWTTGETLPPKYLHYDPETG-----HQLLCDKCAPGTYLKQHC--TVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cowpox virus (CPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
                                                                                                                                                                                              25 YAPSNGKCKDNEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACL
                                                                                                                                                                           31 YDPETG------HQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECV
                                                                                                                                                                                                                                                                                                                                                EATQKCGIDVTL----CEEAFFR--FAVPTKIIPNWLSVLVDSLPGTKVNAESVERIKR-
                                                                                                                                                                                                                                                                                                                                                                                                      ------RHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDL---CESSVQRHLGHS
                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 349;
                                                                                                                       Length 349;
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                                                                                                                      ; Score 224; DB 12; Length 3; Pred. No. 5.2e-10; 41; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MUNICH OPV89/5(CAT), MUNICH OPV 91/1(CAT);
Loparev V. N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, U90223; AAB94389.1; -.
EMBL, U90228; AAB94384.1; -.
                                                                               8630EFAED7A584B5 CRC64;
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; 38063 MW; 424EE08FDEDD04CF CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00020; TNFR_C6; 2.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
PROSITE; PS50050; TNFR_NGFR_2; 1.
PRODOM; PD000771; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
          INTERPRO; IPRO01368; -.
PFAM; PF00020; TNER_c6; 2.
PROSITE; PS00620; TNER_NGFR_1; 2.
PRODOM; PD000771; -; 1.
SEQUENCE 349 AA; 37978 MW; 86
                                                                                                                    Query Match 10.3%;
Best Local Similarity 24.9%;
Matches 76; Conservative 4
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Best Local Similarity
HSSP; P25942; 1CDF
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 1, 2001, 09:16:58; Search time 70.93 Seconds Run on:

(without alignments)
193.313 Million cell updates/sec

US-09-389-782A-2 2179 1 MNKWLCCALLVLLDIIEWTT......QKLFLEMIGNQVQSVKISCL 401 Title: Perfect score: Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

268485 seqs, 34193795 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

/SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Mouse osteoprotege	Rat osteoprotegeri	Tumour necrosis fa	Tumour necrosis fa	Human FTHMA-070 pr	Full length osteoc	Human OCIF genome	Human osteoprotege	Osteoprotegrin pro	TR1 receptor prote	Mutated OCIF, OCIF	Mutated OCIF, OCIF
Ω	W38344	W38343	Y05742	W95030	W83926	R99925	W53239	W38345	Y43400	W57635	R99932	R99931
	18	18	20	20	20	17	19	18	21	19	17	17
% Query Match Length DB	401	401	401	401	401	401	401	401	401	401	401	401
å Query Match	100.0	95.4	87.2	87.2	87.2	87.0	87.0	86.8	86.8	86.8	86.5	86.5
Score	2179	2079	1900	1900	1900	1895	1895	1892	1892	1891	1885	1885
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Mutated OCIF, OCIF Mutated OCIF, OCIF Mutated OCIF, OCIF Mutated OCIF, OCIF Human OCIF genome Modified TR1 recep Mutated OCIF, OCIF MUTATED MU	si si si si	ALIGNMENTS diagnosis; affinity purification; diagnosis; affinity purification; probe; detection; screening; mouse; Paget's disease; hypercalcaemia; ttoid arthritis; osteonyelitis; codontal bone loss; bone necrosis; alifiers	
R999942 R099934 R099933 R099935 R099948 R099936 R099939 R099933 R099943 R099943 R099943 R099944 R099944	ϕ	ALIGNMENTS n; 401 AA. ry) dy; diagnosis; aff transgenic animal de; probe; detecti sis; Paget's disea eumatoid arthritis periodontal bone 1 n/Qualifiers 5 a t= osteoprotegerin	
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88888888866		standard; 1998 (fi steoprote otegerin; nant prod sease; os rathyroid tic metas enia; mur	1996; 1996; 1995; AMGEN
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0.000000000000000000000000000000000000	00000000000000000000000000000000000000	RESULT W38344 ID W38344 ID W38. XX W38. XX DT 20-2 XX DE W0000 XX DO W00000 XX DO W000000 XX DO W000000000 XX DO W00000000000000000000000000000000000	(A) 20 20 4 20 4 20 4 20 4 20 4 20 4 20 4
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The present sequence is rat osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the cDNA can be used as probes to detect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or operate thom diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis, osteomyelitis, ;, osteopytic metastases, periodontal bone loss, bone necrosis and
 prevention;
               antisense oligonucleotide; probe; detection; screening;
bone disease; osteoporosis; Paget's disease; hypercalcaemia;
hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
osteolytic metastasis; periodontal bone loss; bone necrosis;
                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding osteoprotegerin - useful for treatment
                                                                                                                                                                                                                                                                                                                                                                                     diseases involving excessive bone loss, e.g. osteoporosis
   transgenic animal; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.4%; Score 2079; DB 18; 94.5%; Pred. No. 8.5e-171; iive 10; Mismatches 12;
                                                                                                                                                                                                                                                                                               Chang MS;
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Pages 102-104; 182pp; German.
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recombinant production;
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Best Local Similarity
Matches 379; Conserv
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                                                                                                     Rattus sp.
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                                                                                                                                                       The present sequence is mouse osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the cDNA can be used as probes to detect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or osteoporosis, Paget's disease, hypercaleania, osteomyelitis, osteoporosis, Paget's disease, hypercaleania, osteomyelitis, osteopytic metastases, periodontal bone loss, bone necrosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
                                                                                     treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 401;
                                                                                    Nucleic acid encoding osteoprotegerin – useful for treatme
diseases involving excessive bone loss, e.g. osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2179; DB 18;
100.0%; Pred. No. 2.1e-179;
ive 0; Mismatches 0;
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                                                                                                                             Claim 23; Pages 106-107; 182pp; German.
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               Lacey
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             Calzone FJ,
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Best Local Simi
Matches 401;
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180 300 300 360 LCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLK 120 **9**0 Gabs KRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQL&ALME 1 MNKWLCCALLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKT HRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNAT HDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVERI SLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPKT Length 401; Indels

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1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
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Identifying agonists and antagonists of tumor necrosis factor related receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of cancer, AIDS, Alzheimer's disease, bone disease etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection, stroke, ischaemia, acute respiratory disease syndrome,
                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor; TRI; osteoprotegerin; agonist; antagonist; screening; human; cancer; ALDS; Alzbelmer's disease; inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury; bone disease; atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.
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                                                                    361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL
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                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor TR1.
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                                                                                                                                                                      Y05742 standard; Protein; 401
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                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                        19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Gaps

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Length 401; Indels

87.2%; Score 1900; DB 20; 85.8%; Pred. No. 2.1e-155; iive 26; Mismatches 29;

Query Match 87.2 Best Local Similarity 85.8 Matches 345; Conservative

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Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis; inflammation; septicemia; autoimmune disease; transplant rejection; graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome;, restenosis, bone disease; cancer; athersclerosis; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TL5
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                                                            60 TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL
                                                                                                                                                                                                                                                                                          ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK
                                                                                                        120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA
                                                                                                                                                                     180 THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis factor receptor (TNF-R) related polypeptide TRL.
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                                                                                                                                                                                                                                                                                                                                                    Page 11-12; 18pp; English.
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97US-0056980.
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26-AUG-1997;
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10-OCT-1997;
18-APR-1997;
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or TL4 with a candidate compound in the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia,
                                               autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, athersclerosis and Alzheimer's disease. The present sequence represents a TNF R related
                                                                                                                                                                                                                                                  KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                                                                                                                                                                                            THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER 239
                                                                                                                                                                                                                                                                                                                                    TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
                                                                                                                                                       Gaps
                                                                                                                                                                         1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK 59
                                                                                                                                                                                   IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKI1QDIDLCESSVQRHLGHSNLTTEQLLALM
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                                                                                                                                  Score 1900; DB 20;
Pred. No. 2.1e-155;
; Mismatches 29;
                                                                                                                                   87.2%; Score 1900;
85.8%; Pred. No. 2.
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/label= Mat_protein
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                                                                                                                                                      Conservative
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                                                                                                                                             Similarity
                                                                                                        401 AA;
                                                                                     polypeptide TR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  having homology to tumour necrosis factor receptor. The sequence was deduced from that of a cDNA clone (see V69277) isolated from a cardiac coronary artery smooth muscle cell library. FTHMA-070 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for identifying compounds which bind to or modulate the activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological disorders.
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                                                                                                                                                                                                                                                                                         New isolated human FTHMA-070 and T85 proteins - used to develd products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.
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85.8%; Pred. No. 2.1e-155;
ive 26; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 1; 127pp; English.
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97US-0062017.
97US-0044746.
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Best Local Similarity 85.8
Matches 345; Conservative
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                                                                                                                                                  McCarthy
                                                                                                                                                                                                         WPI; 1999-024021/02.
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                                                                                                                                                                                                                                     N-PSDB; V69277
                                                                                                                                                  Holtzman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1997
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ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK
                                               WPI; 1998-169150/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V20768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MONS ( MONS)
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    WO9807840-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1997;
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                                                                                                                                                                                         15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sclerosis
                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
                                   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. outseful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding osteoclastogenesis inhibitory factor protein - useful bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 1895; DB 17;
85.6%; Pred. No. 5.6e-155;
iive 26; Mismatches 30;
          Full length osteoclastogenesis inhibitory factor.
                                                                                                                                                                                                                                                                                                                   Mochizuki S,
a M, Yano K,
                                                                                                                       /note= "Signal peptide"
22..401
/note= "Mature OCIF, claim 6"
                                                                                                                                                                                                                                                                                                                   F, Mochi
Ueda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 64-66; 183pp; Japanese
                                                                                                                                                                                                                                                                                            (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                   Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                     Kobayashi
                                                                                                                                                                                                                                                                                                                                  Tsuda E,
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95JP-0054977
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                                                                                                                                                                                                                                                                                                                   Soto M, Higashio K,
Nakagawa N, Shima N,
                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-402320/40.
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                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T36685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis.
                                                 osteoporosis
                                                                          Homo sapiens
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                                                                                                                                                                            WO9626217-A1
                                                                                                                                                                                                                            20-FEB-1996;
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20-FEB-1995;
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                                                                                                                                                                                                                                                                                                                     Goto M,
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The present sequence represents human OCIF genome DNA protein which is specifically claimed in the present invention. The present invention describes: (1) a method of inhibiting the formation of osteoclasts and/or antipyretic proteins, which have the following characteristics: (1) MW determined by SDS-PAGE of approximately 60 kDa under reducing conditions, and 60 kDa and 120 kDa under non-reducing conditions; (11) (see W5229); (11) affinity to cation exchangers and heparin; (1v) its osteoclast formation inhibiting activity reduced by heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius for 10 minutes or 56 degrees Celsius (20 30 minutes, and (2) a method for preparing the sologous proteins. The proteins are useful for, e.g. treatment and prevention of osteoporosis, rheumatism or multiple sclerosis, and also as antigens for immunological diagnosis of these diseases and disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition of osteoclast formation and/or antipyretic activity useful for, e.g. treating osteoporosis, rheumatism and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                             Human; OCIF; genome; osteoclast; antipyretic; osteoporosis; rheumatism; multiple sclerosis.
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85.6%; Pred. No. 5.6e-155;
tive 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..21
/label= signal
22..401
/label= OCIF_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                     Human OCIF genome DNA protein.
W53239 standard; Protein; 401
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                                                                                                                                  (first entry)
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Best Local Similarity 85.6
Matches 344; Conservative
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(AMGE-) AMGEN INC
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                                          KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                             240 IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 299
                                                                                                                                                                         ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK 359
                                                                                                                                                                                  180 THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER
                                                                                                                                                MNKWLCCALLVLLDI - IEWTTOETLPPKYLHYDPETGHOLLCDKCAPGTYLKOHCTVRRK
         60 TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL
                                                                                                                                                                                                                                                                                                                                                 prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for treatment of e.g. osteoporosis
                                                                                                                                                                                                                                                                                                                                      Osteoprotegerin; antibody; diagnosis; affinity purification; recombinant production; transgenic animal; treatment; preventic antisense oligonucleotide; probe; detection; screening; human; bone disease; osteoprosis; Paget's disease; hypercalcaemia; hyperparathyroidism; rheumatcid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; bone necrosis;
                                                                                                                                                                                                        Nucleic acid encoding osteoprotegerin - useful diseases involving excessive bone loss, e.g. os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang
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                                                                                                                                                                                                                                                                      A.
                                                                                                                                                                                                                                                                      Protein; 401
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                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FJ,
                                                                                                                                                                                                                                                                                                                        Human osteoprotegerin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-334271/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calzone
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                                                                                                                                                                                                                                                                      W38345 standard;
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Osteoprotegrin; OPG; human; cardiovascular disease; occlusion; calcification; blood vessel; atherosclerosis; medial calcific sclerosis; Monckeberg's arteriosclerosis; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA
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recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the CDNA can be used as probes tdetect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or prevent bone diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss, bone necrosis and
                                                                                                                                                                                                                                                                                                                                                     Length 401;
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                                                                                                                                                                                                                                                                                                                                                       86.8%; Score 1892; DB 1885.6%; Pred. No. 1e-154;
                                                                                                                                                                                                                                                                                                                                                                                                   26; Mismatches
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                                                                                                                                                                                                                                      osteopaenia.
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                                                                                                                                                                                                                                                                                      Sequence
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WO9812344-A1. Homo sapiens

18-SEP-1996;

26-MAR-1998

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                                                                                                                                                             This sequence represents the human osteoprotegrin (OPG). The invention relates to a method of treating or preventing cardiovascular disease by administering OPG. The method can be used to treat and prevent cardiovascular diseases associated with occlusion and calcification of blood vessels, especially atherosclerosis or Monckeberg's arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or prevent cardiovascular diseases provides an alternative to invasive treatments. OPG can be used as a single therapeutic for prevention and treatment of both osteoporosis and cardiovascular diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                              60 TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM
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Pred. No. 1e-154;
                                                                                    Treating and preventing cardiovascular diseases, \epsilon atherosclerosis and Monckeberg's arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL
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                                                                                                                                   9; Page 37-39; 43pp; English.
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85.6%;
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               Sarosi I;
                                          WPI; 2000-013182/01
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                         N-PSDB; Z37254
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              Simonet S,
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                                                                                                                                   Claim
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the Internation in the line a vector, which is then used to transfect the host cell. The TRI receptor can bind both TNF-alpha and TNF-beta. TRI receptor and bind both TNF-alpha and TNF-beta. TRI receptor agonists can be used for inhibition of tumour growth and necrosis of tumours. They can also be used to stimulate cellular differentiation, e.g. T cell, fibroblasts or haematopoietic cell differentiation, may be used to augment TRI's role in the host's defence against microorganisms and prevent related disease. The agonists may also be used to protect against the deleterious effects of ionising radiation produced during a course of radiotherapy, e.g. denaturation of enzymes, lipid peroxidation or DNM damage. The agonists may further be used to mediate an anti-viral response, to regulate growth, to mediate the immune response and to treat immunodeficiencies related to diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as HIV. Antagonists to the TRI receptor may be used to treat autoimmune diseases, e.g. graft versus host rejection and allograft rejection, and T cell mediated autoimmune diseases. They may also be used to prevent apoptosis. They may also be used to prevent apoptosis. They may also be used to treat septic shock, meningococcemia, inflammation, bacterial infections, cachexia, cerebral malaria or AIDS. The products can also be used for diagnosing the above diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
                                                                                                                                                                                                                                                                                                                     New isolated tumour necrosis factor receptor - useful for developing products for treating, e.g. tumours, auto-immune disease(s), graft rejection, apoptosis or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention. The DNA can be used to produce a recombinant host
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                                                                                                                                                                                                                                                                                                                                                                                                                               is a tumour necrosis factor receptor-1 (TR1)
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                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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Matches 343; Conserv
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KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA
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                                                           1 MNKWILCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
               Mutated OCIF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis
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20-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
  ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK 359
             Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deg.C. OCIF is useful in the contion of disorders of bone resorption, e.g. in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding osteoclastogenesis inhibitory factor protein-
bone resorption control, esp. treatment of osteoporosis
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Yasuda H;
                                             TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
                                                        F, Mochizuki S,
Ueda M, Yano K,
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note= "Mature OCIF-C205"
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Tsuda E,
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95JP-0054977.
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N, Shima N,
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20-FEB-1995;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorptio
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Yasuda H;
Mochizuki S,
la M, Yano K,
                                                                                                                                                                                             /note= "Mature OCIF-C19S"
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                                                                                                                                                                            /note= "Signal peptide"
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Nakagawa N, Shima N,
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Gaps

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401;

Length Indels

86.5%; Score 1885; DB 17; 85.3%; Pred. No. 4.1e-154; ive 26; Mismatches 31;

Best Local Similarity 85.3 Matches 343; Conservative

Query Match

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20-FEB-1996;
                            21-JUL-1995;
20-FEB-1995;
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                                                                                        Nakagawa
                                                                                                                                                                                                                                                                                                               Sequence
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              osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C195 in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. Co 30 mins at 56 deg. C, and is lost after 10 mins at 70 deg. Co CIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                 120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
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         version of the full length
                                                                                                                                                           Length 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.5%; Score 1885; DB 17;
85.3%; Pred. No. 4.1e-154;
ive 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mature OCIF-CL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Signal peptide"
22..399
/note= "Mature OCTF-CT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
         sequence represents a mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R99942 standard; Protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                             343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutated OCIF, OCIF-CL
                                                                                                                                                                   Local Similarity
                                                                                                                             Š
                                                                                                                            401
                                                                                                           osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis
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                                                                                                                             Sequence
                                                                                                                                                           Query Match
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                                                                                                                                                                  Best Loca
Matches
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osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deg.C. OCIF is useful in the control of bone resorption and uncreasing the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSHFPK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a mutated version of the full length
                                                                                                                                                                                      Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
                                                                                                                                                                                                                                                                                                                                         DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                 Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                   F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.4%; Score 1882; DB 17;
85.5%; Pred. No. 7.3e-154;
iive 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 62; Page 117-119; 183pp; Japanese.
                                                                                                                                  (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                      Kobayashi
                                                                                                                                                                                                                 Tsuda E,
                                                95JP-0207508.
96WO-JP00374
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Best Local Similarity 85.5
Matches 342; Conservative
                                                                                                                                                                                   Higashio K,
N, Shima N,
                                                                                                                                                                                                                                                               WPI; 1996-402320/40.
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IKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALM
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                                                                                                                                                                                                                                                                                                                                           osteoporosis
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20-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C225 in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C ocities useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 khrscppgfgvvgagtperntvckrcpdgffsnetsskapcrkhtncsvfgllltgkgna 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 TLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEFCL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVER 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding osteoclastogenesis inhibitory factor protein - useful bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1880; DB 17;
; Pred. No. 1.1e-153;
26; Mismatches 32;
                                                                                                                                                                             OCIF-C22S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 38; Page 100-102; 183pp; Japanese.
                                                                                                                                                 /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                      (SNOW ) SNOW BRAND MILK PROD CO LID
                                                                                                                         Location/Qualifiers
                                                                                                                                                                           'note= "Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%;
85.1%;
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                                                                                                                                                                                                                                                                                    96WO-JP00374
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95JP-0054977
 (first entry)
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Best Local Similarity 85.18
Matches 342; Conservative
                             OCIF-C22S.
                                                                                                                                                               22..401
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N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-402320/40.
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                             Mutated OCIF,
                                                                     osteoporosis
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20-FEB-1995;
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22-APR-1997
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                                                                                             Synthetic
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                             ESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDODTLKGLMYALKHLKTSHFPK
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Yasuda H;
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                                                                                                                                                                                                                     Kobayashi F, Mochizuki
Tsuda E, Ueda M, Yano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Mature OCIF-C21S"
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                                                                                                                                                                                                                                                                                                                                                                                    R99933 standard; Protein; 401
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N, Shima N,
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                    Gaps
                                             1 MNKWLCCALLVLLDI-IEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRK
Length 401;
                   Indels
                                                                                                                                                                                                                                                                    360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Query Match 86.2%; Score 1879; DB 17; Best Local Similarity 84.8%; Pred. No. 1.3e-153; Matches 341; Conservative 28; Mismatches 31;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
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sp_bacteria:*
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Maximum DB seq length: 200000000
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Q9mxa0 aulonocara 062868 sus scrofa 0946363 sus scrofa 09440 homo sapien 098044 aulonocara 091048 homo sapien 097951 homo sapien 097951 homo sapien 03009 homo sapien 03009 homo sapien 03000 homo sapien 030102 homo sapien 030102 homo sapien 030107 homo sapien 0301467 morone saxa 031467 morone saxa	homo homo moron homo homo
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### ALIGNMENTS

RESULT	0LT 1	
a 2	O9RIA4 PRELIMINARY; PRT; 437 AA.	
턴턴	01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
F E	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	
SC	Mus musculus (Mouse).	
ပ္ပ		
S S	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;	
Z C	[1]	
R &	SEQUENCE FROM N.A. Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;	
RŢ	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal	
E E	antibody (Mab 7, its light and heavy chains) and construction of a	
7 H	single chain ancidedy (serv); Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF152372; AAD40243.1;	
DR	HSSP; P01842; 7FAB.	
ž č	INTERPROT IFROMOSOUS.	
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F. O	NON_TER 437 437 SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;	
бă	Query Match 65.7%; Score 829.5; DB 11; Length 437; Best Local Similarity 61.4%; Pred. No. 5.7e-68;	
Σ̈́	Indels 9; Gaps	m
ΣŽ	2 PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 59	
g	212 PRDCGCKPCICIVPEVSSVFIFPPFKPKDVLIITLTPKVTCVVVDISKDDPEVQ 264	
à	60 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 119	
g	16.1.1   11.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.1   1.	
δy	120 TISKAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 179	

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Gaps

Indels

Length 384;

--- DTLMISRTPEVT, 45

QQ ò g 090544

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CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 EWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 RWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPL 353
                                                                                                                                                                                                                                                                                                                                                                                                    CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 CTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular analysis
                                                            SEQUENCE FROM N.A.
Zheng S., Cao J., Cao W., Cai X., Geng L.;
"Identification and characterization of SNC73, a gene which is
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo
                                                                                                                    regulated in colorectal cancer.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL: AF0674-20; AAC19365.1; --
HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389978; CAB97534.1; -.
                                                                                                                                                              Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBLrel. 15, Last sequence update)
MBLrel. 15, Last annotation update)
HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.2%; Score 268; DB 4; Le Best Local Similarity 32.8%; Pred. No. 1.3e-16; Matches 77; Conservative 34; Mismatches 112;
                                                                                                                                                                                                                                                                                                    21.5%; Score 272; DB 4; I 31.2%; Pred. No. 5.1e-17; ive 33; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                              7 KTHTCP-----PCPAPELLGGPSVFLFPPKPK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Merazoa; Chordata;
Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                            Conservative
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354 AFTQKTIDRLAGK 366
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Matches 79; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 EL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
EMBL; 018701; AB484195.1; -.
HSSP; P01857; IFC1.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 SVFLFPPKPTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYN 82
                                                                                                                                                                                                                                                                                                                         Chondrichthyes;
         Homo sapiens (Human).
Eykaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                               Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 272.5; DB 13; Length 684;
Pred. No. 9.4e-17;
5; Mismatches 98; Indels 9;
                                                            180 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NOVEL ANTIGEN RECEPTOR PRECURSOR.
Ginglymostoma cirratum (Nurse shark).
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostomatidae; Ginglymostomatidae; Ginglymostomatidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOVEL ANTIGEN RECEPTOR.
2FF9D2071CDA6DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                            AA.
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                                                                                                                                                                                          684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; ig; 6.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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MEDLINE-95183140; PubMed=7877689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 21.6%; Sco
1 Similarity 33.3%; Pro
71; Conservative 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  684 NC
75224 MW;
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                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7801;
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SNC73.
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SIGNAL

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Signal

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Gaps

12;

Indels

Length 416;

Q9UP60 Q9UP60;

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Euteleostomi;

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RESULT
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                                                        64 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 123
                                                                                                                 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 HITLDR--SPLRGIANLSNFIRVSPTVKVTQQSPTSMNQVNLTCRAERFYPEDLQLIMLE
4 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                   5 CDKTHTCPPCPAPELL - GGPSVFLF - - - PPK - - - PKDTLMISRTPEVTCVVVDVSH - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CVKFQKGPSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTC----KSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPIEKTISKAKGQPREPQVYTLPPS----RDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                            NGQPENNYKTTPPVL - - DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE - - - ALHNHYT -
                                                                                                                                                                            232
                                                                                                                                                                                                       344 SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGK 398
                                                                                                                                                                           181 PVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00290; IG_MHC; UNKNOWN_1.
509 AA; 55997 MW; 55023F2FC1A002B5 CRC64;
                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%; Score 183; DB 1
25.7%; Pred. No. 1e-08;
iive 42; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sano S., Ohnishi H., Kubota M.;
"Gene structure of mouse BIT/SHPS-1.";
Biochem. J. 344:667-675(1999).
EMBL; AB024507; BAA89289.1; JOINED.
EMBL; AB024507; BAA89289.1; JOINED.
EMBL; AB024501; BAA89289.1; JOINED.
EMBL; AB024503; BAA89289.1; JOINED.
EMBL; AB024503; BAA89289.1; JOINED.
EMBL; AB024503; BAA89289.1; JOINED.
EMBL; AB024504; BAA89289.1; JOINED.
EMBL; AB024505; BAA89289.1; JOINED.
EMBL; AB024506; BAA89289.1; JOINED.
                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129SV; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 LGLAHSSDQGSMQTFPG 365
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Matches
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neurite outgrowth.";
Dev. Biol. 137:219-232(1990).
1-1-FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE
2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
MITOGRNS AND CELL ADHESION. PROTEIN SUPPORTS ADHESION OF
CEREBELLAR NEURONS, NEURITE OUTGROWTH AND GLIAL CELL ATTACHMENT.
MAY PLAY A KEY ROLE IN INTRACELLULAR SIGNALING DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIMARILY ASSOCIATES WITH SHP-1.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE ROCDUCTS: THREE FORMS; ISOFORMS I (SHOWN HERE), 2 AND ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN THE CEREBRAL CORTEX, CEREBELLUM, SPINAL CORD, SPLEEN AND MACROPHAGES AND AT WICH LOWER LEVEL IN THE KIDNEY, HEART, LIVER AND THYMUS. WITHIN THE CEREBELLUM, EXPRESSION IS DETECTED IN THE SYNAPTIC GLOMERUIL, GRANULE CELL BODIES, GOLGI EPITHELIAL CELLS, OLFACTORY BULB, NOUFONS IN THE HPOCAMPUS AND THE DENTATE GYRUS. IN THE EXE, EXPRESSION IS FIRST SEEN IN THE INNER PLEXIFORM AND OPTIC FIBER LAYERS. LATER IN DEVELOPMENT
                P97797; P97796; 035924; 088555; 08856; 01.NOV-1998 (TERBALE-1. 08, Created) 01.NOV-1998 (TERBALE-1. 08, Created) 01.NOV-1998 (TERBALE-1. 08, Last sequence update) 01.OCT-2000 (TERBALE-1. 15, Last annotation update) PROTEIN TYROSINE PHOSFHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR (P84) (SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS-1) (SHPS-1) PPNS1 OR P84 OR SHPS-1 OR SHPS-1 OR SHPS-1 OR SHPS-1 OR SHPS-1 OR PATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 32-53; 422-424 AND 429-433. STRAIN=BALB/C; TISSUE-CREBELLUM, AND BRAIN; Comu S., Weng W., Olinsky S., Ishwad P., Mi Z., Hempel J., Watkins & Lagenaur C.F., Narayanan V.; The murine P84 neural adhesion molecule is SHPS-1, a member of the
                                                                                                                                                                                                                                                                                                                                                                                     Pulloka x., kasuga m.; Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            association";
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

BEDLINE-20152134; PubMed=2303162;

Chiang W., Lagenaur C.F.;

"Central nervous system antigen P84 can serve as a substrate for
                                                                                                                                                                                                                                                                                                                                              Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi
Fujioka Y., Kasuga M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHPS-1 and its
in macrophages
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513 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=129SV; TISSUE=LIVER;
Sano S., Ohnishi H., Kubota M.;
"Gene structure of mouse BIT/SHPS-1.";
Biochem. J. 344:667-675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphatase-binding protein family.";
J. Neurosci. 17:8702-8710(1997).
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  PRT;
                                                                                                                                                                                                                                                                                                                                  MEDLINE=97223399; PubMed=9070220;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              localization of genes."
                                                                                                                                                                               Wus musculus (Mouse)
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN;
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EXPRESION IS ALSO SEEN IN THE OUTER PLEXIFORM, RETINA AND OUTER SEGMENTS OF THE PHOTORECEPTOR LAYER.

DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 7, WHEN EXPRESSION IS RESTRICTED TO THE FLOOR PLATE REGION OF THE VENTRAL NEURAXIS. WIDESPREAD TO THE FLOOR PLATE REGION OF THE VENTRAL STARRALS. WIDESPREAD EXPRESSION IN A VARIETY OF CNS REGIONS BEGINS SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS TWO C1-LIKE AND ONE V-LIKE DOMAINS.

L; DB9766, BAAA13521.1; -
L; D87967, BAAA13521.1; -
L; D87967, BAAA13521.1; -
L; U89694, AAB92591.1; -
                                                                                                                                                                                                                                                           PFAM, PF00047; 1g; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Signal; Transmembrane; Alternative splicing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY CAMP) (POTENTIAL). (BY TYR-KINASES)
                                                                                                                                                                                                                                                                                                                    PROTEIN TYROSINE PHOSPHATASE, NON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
MISSING (IN ISOFORM SMALL)
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                               RECEPTOR TYPE SUBSTRATE 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C1-TYPE DOMAIN.
IG-LIKE C1-TYPE DOMAIN.
IG-LIKE C1-TYPE DOMAIN.
SH2-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 -> L (IN REF. 2).

7 -> A (IN REF. 2).

7 -> R (IN REF. 3).

5 -> P (IN REF. 3).

5 -> P (IN REF. 3).
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                                                                                                                                                                                                                                                                                            Glycoprotein; SH3-binding; Phosphorylation. SIGNAL
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                                                                                                                        EMBL; AF072543; AAC24886.1; EMBL; AF072544; AAC24887.1; EMBL; AB024507; BAA89290.1; JOINED. EMBL; AB024501; BAA89290.1; JOINED. EMBL; AB024501; BAA89290.1; JOINED. EMBL; AB024503; BAA89290.1; JOINED. EMBL; AB024504; BAA89290.1; JOINED. EMBL; AB024505; BAA89290.1; JOINED. EMBL; AB024505; BAA89290.1; JOINED. EMBL; AB024505; BAA89290.1; JOINED. EMBL; AB024505; BAA89290.1; JOINED.
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INTERPRO; IPR003006; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: | :| : | :| 233 HITLDR--SPLRGIANLSNFIRVSPTVKVTQQSPTSMNQVNLTCRAERFYPEDLQLIWLE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 PAPIEKTISKAKGQPREPQVYTLPPS-----RDELTKNQVSLTCLVKGFYPSDIAVEWES 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 NGQPENNYKTTPPVL--DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT- 222
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          CDKTHTCPPCPAPELL--GGPSVFLF----PPK---PKDTLMISRTPEVTCVVVDVSH-- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLR)
01-OCT-2000 (TrEMBLR)
Ginglymostoma cirratum (Nurse shark).
Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95183140; PubMed=7877689;
Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                           14.5%; Score 183; DB 11; Length 513; 25.7%; Pred. No. 1e-08; ive 42; Mismatches 107; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greenberg A.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U18680; AAB48352.1; -.
INTERRO; IPRO33006; -.
PROSITE; PS00297; IG. ALC; UNKNOWN_1.
NON_TER 268 AA; 29579 MW; OCDE524DD6E9FDC4 CRC64;
                A -> T (IN REF. 2 AND 3).
E -> A (IN REF. 3).
T -> I (IN REF. 3).
KG -> KG (IN REF. 2).
P -> S (IN REF. 2).
H -> P (IN REF. 3).
L -> F (IN REF. 3).
L -> F (IN REF. 3).
C -> F (IN REF. 3).
KG -> M (IN REF. 2).
KG -> M (IN REF. 3).
    3).
2 AND
2 AND
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                                                                                                                                                                                                                                                          56424
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91
114
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Best Local Similarity
Matches 66; Conserv
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Q90524;
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176 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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                                                                                                                                                                                                                                                                                                             "BIT (Bit) maps to mouse chromosome 2."; denomics 40:504-506(1997).
EMBL; D85785; BAA20376.1; -.
MGD; MGI:107947; Bit.
                                                                                                                      04, Created)
04, Last sequ
15, Last anno
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MEDLINE-97230468; PubMed-9073522;
Ohnishi H., Kubota M., Sano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
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06,
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Best Local Similarity 27.75
Matches 66; Conservative
                                                                                            PRELIMINARY;
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                                                                                                                 01-JUL-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                   IPR003006;
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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046631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 PIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 EFKSGPGTHLTVNAKPSPPVVSGPTV------RATPEQTVNFTCTSHGFSPRN 179
                                                                                                                   67 -----VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV--SNKALPAP 116
                                                                                                                                                                                        :| :| :| :| :| | 1.3 | :| | 1.4 LEELDWIXVYGGGTGVTVNPGIPLSPPIVSLLHSATEEQRANGFVQLVCLISGYYPENIA 173
                                                                                                                                                                                                                              164 VEWESINGOP-ENNYKITPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT 222
                                                                                                                                              66 TISKGGRYVETVNSGSKSFSLRIND-----LTV-----EDSGTYRCKVYRKNWAYDCG 113
                                                                                                                                                                          IEKT------ISKAKGQPREPQVYTL--PPSRDELTKNQVSLTCLVKGFYPSDIA 163
                                                                                                                                                                                                                                                      174 VSWQKNTKTITSGFATTSPVKTSSNDFSCASLLKVPLQEWSRGSVYSCQVSHSATSSNQR 233
                                        Gaps
                                                                  99
                                                                                          65
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYVF-----TARVDQTPQEITKETGESLSINCVLRDSNCALPSTYWNRKKSGSTNEE
                                                                23 PSVFLFPPKPKDTLMISRTPE-----VTCVVVDVSHEDPEVKFNWYVDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                        90;
              Length 268;
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                                       Indels
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MYD-1 ANTIGEN.
ACDDEEA9C9708A82 CRC64;
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Last annotation update)
                                       90;
              DB 13;
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            14.3%; Score 181; DB 1.
25.1%; Pred. No. 7e-09;
                                       35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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506 MY
55117 WW;
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EMBL; Y11045; CAA71942.1; -.
INTERPRO; IPRO03006; -.
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                                       Conservative
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27
506 AA;
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                          Similarity
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234 KEIRSTS 240
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72 AKTKPREEQYNSTYRVVS-VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR- 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 SPTVKVTQQPPT----SMNQVNLTCRAERFYPEDLQLIWLENGNVSRN--DTPKNLTKNT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 GGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTC----KSHGFSPRNITLKWFKDGQELHP 194
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TISSUB-PERIPHERAL BLOOD;
MEDLINE-98143722; PubMed-9485180;
Brooke G.P., Parsons K.R., Howard C.J.;
"Cloning of two members of the SIRP alpha family of protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GGPSVFLF----PPK---PKDTLMISRTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVHN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT-----QKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 509;
297 EAASVLVENKDGTFNQTSWLLVNSSAHREAVVLTCQVEHDRQPAVSKNHT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FOO AA; 56033 MW; IE377ACEC31BA13E CRC64;
                                                                                                                                                                                                                                                                           ul-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) BRAIN IMMUNOLOGICAL-LIKE PROTEIN (BIT).
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Last annotation update)
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SNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVYTLPPS-----RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL--D 184
                                                                  56 PEVKFNWYVDGV-EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 PYVF-----TARVDQTPRSVTKETGESLTINCVLRDASYALGHTCWFRKKSGSTKEE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GGPSVFLF----PPK----PKDTLMISRTPEVTCVVVDVSH--EDPEVKFNWYVDGVEVHN 71
         ----ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.6%; Score 171.5; DB 11; Length 25.8%; Pred. No. 1.1e-07; Live 39; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse type III BIT.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB108194; BAA76555.1;
INTERPRO; IPRO03006;
PFAM; PF00047; 19; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 509 AA; 55986 MW; CF5A6EC9404C14CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
         ---- ATCVVVDVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||:: | |::| :::|
TDGTYNYTSLFLVNSSAHREDVVFTCQVKHDQQPAITRNHT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                      509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9MXA2;
01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
         PSVFLFPPKPKDTLMISRTPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2000 (TrEMBLrel. 15, BIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.84
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                227 SLS 229
                                                                                                                                                                                                                                                                            STS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sano S.;
                                                                                                                                                                                                                                                                                                                                                      Q9WTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9MXA2
                                                                                                                                                                                                                                                                                                                        RESULT 12
         23
                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                        Q9WTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9MXA2
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&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
phosphatase binding proteins in cattle that are expressed on monocytes and a subpopulation of dendritic cells and which mediate binding to CD4 T cells.";
                                                                                                                                                                                                                                                                               58 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA-- 115
                                                                                                                                                                                                                                                                                                                                                    180 ISLKWFKNGNELSASQTSVDPEDNNVSYSINSTTKVLLATGDVHSQVICEVAHVTLQGGP 239
                                                                                                                                                                                                                                                                                                                                                                                  116 PIEKTISKAKGQPREPQVYTLPPSRDELT----KNQVSLTCLVKGFYPSDIAVEWESNG 170
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                              EPKSCDKTH-TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH--EDPE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 NMSRTEAASVFVENKDGTFNQTSWFLVNSSAHREAVVITCQVEHDGQPAVSKNHT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                          171 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 13.6%; Score 171.5; DB 13; Length 259;
1 Similarity 25.1%; Pred. No. 5e-08;
61; Conservative 30; Mismatches 95; Indels 57;
                                                                                                                                                                                                   Length 506;
                                                                                                                                                                                                 ; Score 175; DB 6; Length 50; Pred. No. 5.4e-08; 36; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greenberg A.S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           POTENTIAL.
MYD-1 ANTIGEN.
6B7E310677FCF9CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28245 MW; 07F9860A92318B6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-COT-2000 (TrEMBLrel. 15, Last annotation update)
NOVEL ANTIGEN RECEPTOR (FRAGMENY).
Ginglymostoma cirratum (Nurse shark).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U1868; AAB48358.1;
INTERPRO; IPR003006;
PFAM; PF00047; 1g; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95183140; PubMed=7877689;
                                                Eur. J. Immunol. 28:1-11(1998).
EMBL: Y11046; CAA71943.1; -.
INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 3.
                                                                                                                                                         55092 MW;
                                                                                                                                                                                                   Query Match
Best Local Similarity 26.4%;
Matches 62; Conservative 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-235 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY; ·
                                                                                                                             26
506
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27
506 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-SPLEEN;
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                                                                                                                                           CHAIN
SEQUENCE
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Best Local Signatches 61,
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SEQUENCE
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                                                                                                              Signal
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us-09-389-782a-1.rspt

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PS00290; IG_MHC; UNKNOWN_1.
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Submitted (DEC-1994)
                257
257 AA:
                                                              Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95183140;
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SPLEEN;
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NON_TER
SEQUENCE
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Best Local Si
Matches 56,
              NON_TER
SEQUENCE
   PROSITE;
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                                                                                                                                                                                                                                                                             RESULT 15
Q90545
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                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                          Murray B.W., Shintani S., Sueltmann H., Klein J.;
"Major histocompatibility complex class II A genes in cichlid fishes: Identification, expression, linkage relationships, and haplotype
                                                                                                                                                                                                                                                                                                                                                                            QDWLNGKEYKCKVSNKALPAPIEKTISKA-KGQPREP-----QVYTLPPSRDEL---TK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                            VTCVVVDVSHEDPEV-----KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 95
                                               Aulonocara hansbaenschi.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei.
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes; Labroidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ginglymostoma cirratum (Nurse shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostomatidae; Ginglymostomatidae
                                                                                                                                                                                                                                                                                                                                               11 VLCVSADVLHEDIQIVGCSDSDGEEMYGLDGEEKAYADFNKKEEIYPQPPFVVNPFH--Y
                                                                                                                                                                                                                                                                                                                                                                                                                           NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
                                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenberg A.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U18693; AAB48364.1; -.
INTERPRO; LERRO30065. -.
PFAM; PF00047; 1g; 2.
                                                                                                                                                                                                 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF212849; AAF65676.1; -
                                                                                                                                                                                                                                      3D18BF05BF0A9C53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                            13.4%; Score 169; DB 7; llarity 29.9%; Pred. No. 7.6e-08; Conservative 27; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 NVFSCSVMHEALHNHYTQ-----KSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL ANTIGEN RECEPTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=SPLEEN;
MEDLINE=95183140; PubMed=7877689;
                                                                                                                                                                                                                                        26005 MW;
01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, MHC CLASS II ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-242 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                 Cichlidae; Aulonocara.
NCBI_TaxID=27781;
                                                                                                                                                                                                                                        238 AA;
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE-SPLEEN;
                                    MHC-AUHA-DBA.
                                                                                                                                                                                         variation.";
                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new ant
                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                      SEQUENCE
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Q90536
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97 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL--PPSRDELTKNQVSLTCLV 154
                                                                                                                                                                                                                                                                             155 KGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KGQPREPQVYT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LIHSATEEQRANRFVQLVCLISGYYPENIAVSWQKNTKTITSGFATTSPVKTSSNDFSCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 L--PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LTV-----EDGGTYRCGVGQYRGCPYFLCSHLSYAGCGDGTVVTVNPGIPPSPPIVS 121
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 VTCVVVDV------SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ginglymostoma cirratum (Nurse shark).
Bukaryota, Wetazoa, Chordata, Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWAVGGAYAAVGDGTA-----VTVNPGIPPSPPIVSLLHSATEEQRANRFVQLVCLI
                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
                                                                         Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 237;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
28083 MW; BAD019A99D0BC491 CRC64;
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Last annotation update)
                                                                         DB 13;
                                                                                                                           64;
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25.8%; Pred. No. 1.8e-07;
iive 32; Mismatches 83;
                                                                      13.2%; Score 166.5; DB 1:
llarity 29.4%; Pred. No. 1.4e-07;
Conservative 21; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AA.
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PROSITE; PS00290; IG_MC; UNKNOWN_1.
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 2.
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Search completed: March 1, 2001, 09:20:02 Job time: 400 sec

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March 1, 2001, 09:13:22 ; Search time 40.97 Seconds
    (without alignments)
182.871 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                OM protein - protein search, using sw model
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US-09-389-782A-1 1263 1 EPKSCDKTHICPPCPAPELL......MHEALHNHYTQKSLSLSPGK 232 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 Total number of hits satisfying chosen parameters:

88757 seqs, 32294092 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01857 homo sapien	homo	P01859 homo sapien	homod	oryct	P01862 cavia porce	_	P20761 rattus norv	P03987 mus musculu	P01868 mus musculu	P20759 rattus norv	P01869 mus musculu	P20762 rattus norv	P01863 mus musculu	P01864 mus musculu	P01865 mus musculu	P20760 rattus norv	P01866 mus musculu	P01867 mus musculu	P01871 homo sapien	mus m	P04220 homo sapien	P06336 mus musculu	P01855 rattus norv	P01854 homo sapien	P01873 mus musculu	P03988 oryctolagus	P04221 oryctolagus	P01874 canis famil	P06337 mesocricetu	P20768 suncus muri	P23085 heterodontu	P01879 oryctolagus
SUMMARIES	ID	GC1_HUMAN	GC3_HUMAN	GC2_HUMAN	GC4_HUMAN	GC_RABIT	GC2_CAVPO	GC3_MOUSE	GCB_RAT	GC3M_MOUSE	GC1_MOUSE	GC1_RAT	GC1M_MOUSE	GCC_RAT	GCAA_MOUSE	GCAB_MOUSE	GCAM_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	MUC_HUMAN	MUC_MOUSE	MUCB_HUMAN	EPC_MOUSE	EPC_RAT	EPC_HUMAN	MUCM_MOUSE	MUC_RABIT	MUCM_RABIT	MUC_CANFA	MUC_MESAU	MUC_SUNMU	HVC2_HETFR	ALC_RABIT
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287.5	287.5	278.5	276.5	272	272	268.5	268	248.5	245.5	177.5	172	
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# ALIGNMENTS

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SULT 1 LHUMAN GC1_F P0185 21-JC 21-JC 21-JC 21-JC IG GP IG GP	OS Homo sapiens (Human).  OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  RN [1]  RP SEQUENCE FROM N.A.  RR MEDLINE-82274238; PubMed-6287432;  RR Ellison J.W., Berson B.J., Hood L.E.;  RT "The nucleotide sequence of a human immunoglobulin C gammal gene.";  RL Nucleic Acids Res. 10:4071-4079(1982).	RX MEDLINE-71064024; PubMed-5489771; RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., RA Waxdal M.J., Edelman G.M.; RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; RL Biochemistry 9:3161-3170(1970).	- የጆጜፀ፣ 40 ቸ	-wzg= eodz-	- N Z N = N H — O Z D = H

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                                                                                                                                                                                                                                   RESIDUES
                                                                                                                                                                                                                                           RESIDUES
                                                                                                                                                 and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
Biochemistry 20:2361-2370(1981).
-!- MISCELLANEOUS: NIE HAS THE GIM 17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.
-!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
                                                                                                                                         "Crystallographic refinement and atomic models of a human Fc fragment
                                               "Rule of antibody structure. The primary structure of a monoclonal IGG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                             MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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K -> R (IN GLM(3) MARKER).
/FIId-VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FIId-VAR_003887.
L -> M (IN GLM(NON-1) MARKER).
/FIId-VAR_003888.
REMOVED POST-TRANSLATIONALLY.
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
                            MEDLINE-77070267; PubMed-1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
                                                                                                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
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HINGE.
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Biochemistry 9:3188-3196(1970)
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PROSITE; PS00290; IG_MHC; 2.
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1FC1; 15-JUL-92.
1FC2; 15-JUL-92.
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121 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDINES-77118861; Pubmed-402363;
Michaelsen T.E., Franded-402463;
"Primary structure of the / hinge' region of human 1gG3. Probable
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30-MAY-2000 (Rel. 39, Last annotation update)
1G GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).
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100.0%; Pred. No. 3.2e-95;
ive 0; Mismatches 0;
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MEDLINE-81021548; PubMed-6774747;
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21-JUL-1986 (Rel. 01, Last seq
30-MAY-2000 (Rel. 39, Last anno
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Matches 232; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION MID ALLO FOR THE THE REGION.
MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANBOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN. MISCELLANBOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAMMA-3 HEAVY CHAINS.
MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
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                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
                                                                                                                                                                                                                                                                                              Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
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                                                                                             MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C., The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
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quadruplication of a 15-amino acid J. Biol. Chem. 252:883-889(1977).
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PROSITE; PS00290; IG_MHC; 1.
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59 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118
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MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human 1962 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
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MEDLINE-81007873; PubMed=6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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E69CBC95705B2F46 CRC64;
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90.5%; Pred. No. 1.2e-86;
iive 13; Mismatches 9;
               /FTId=VAR_003890.
P -> L (IN 0MM).
FTId=VAR_003891.
F -> Y (IN 0MM).
/FTId=VAR_003892.
T -> A (IN 0MM).
/FIId=VAR_003893.
S -> N (IN 0MM).
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F -> Y (IN OMM).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-GMMA-2 CHAIN C REGION.
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/FT1d=VAR_003889.
AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE)
8310878C6878CF9C CRC64;
                                                                                                                                                        Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal
                         of residues 381-391 of human
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Pred. No. 1.1e-85;
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MEDLINE=6964124; PubMed=5782707;
Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                                                        Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank
                                                                            (ZIE)
                                                                            REVISIONS TO 25; 59; 60 AND 264-268
            Hofmann T., Parr D.M.;
"A note of the amino acid sequence immunoglobulins gamma chains.";
MOI. Immunol. 16:923-925(1979).
                                                                                                                                                                                             Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                           MEDLINE=95255298; PubMed=7737190;
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MEDLINE-80114419; PubMed-118920;
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EMBL, V00554; CAA23815.1; --
EMBL, V00554; CAA23816.1; --
EMBL, V00554; CAA23817.1; --
PIR, A02148; G2HU.
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PROSITE; PS00290; IG_MHC; 2.
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Best Local Similarity 91.4%;
Matches 212; Conservative
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SEQUENCE OF 1-121 (DOT)
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326 AA;
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                                                                                               121 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
the
                                   NMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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Catarrhini; Hominidae; Homo.
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Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 ger
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Mammalia; Eutheria; Primates;
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INTERRO; IPR003006; -.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 2.
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35940
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MIM; 147130; -.
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Query Match

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PROSITE; PS00290; IG_MHC; 1.
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SEQUENCE OF 4-68
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MEDLINE=76135469; PubMed=1243651;
MEDLINE=70.
MEDLINE=70.
MEDLINE=70.
Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-84030930; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                      NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 130
                                                                                                                                                                                                                                                        131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 190
                                            Gaps
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                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Sequence studies of the Fd section of the heavy chain of
                                          Indels
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                                        191 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                              286 LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
Pred. No. 7.1e-85;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA CHAIN C REGION.
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                 93.78;
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                                       208; Conservative
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                 Best Local Similarity
Matches 208; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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Pred. No. 1.4e-67;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2 CHAIN C REGION
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                 or send an email to license@isb-sib.ch)
entities requires a license agreement
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Query Match
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P22436;
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                               GC3_MOUSE
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-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
                                                                                                                                                                                                                                                                                                            MEDLINE-71058474; PubMed-4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT 178
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         Birshtein B.K., Hussain O.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
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                                                                                                                                                                                                                                     MEDIINE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                     SEQUENCE OF 134-226.
MEDLINE-7036072. PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig 19G2
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CHAIN).
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25; Mismatches 38; Indels
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                                                                                        Turner K.J., Cebra J.J.;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                 MEDLINE=71058486; PubMed=5538616;
MEDLINE=71058471; PubMed=5538606;
                                                                                                                                                                                                        Biochemistry 13:4796-4803(1974).
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                                                                       SEQUENCE OF 69-133 AND 312-329
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70.4%;
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PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS
                                                                                                                                                                                                                                                                                       MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin C region; Glycoprotein; Transmembrane;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 YFLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-LUL-1999 (Rel. 38, Last annotation update)
1G GAMMA-3 CHAIN C REGION, SECRETED FORM.
329 AA
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HINGE.
PRT;
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STANDARD;
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329 AA;
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                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene."; Cell 18:559-568(1979).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                        EMBL; J00451; AAB59655.1; --
EMBL; V01526; CAA4767.1; ALT_SEQ.
PIR; A02155; G3MSM.
INTERPRO; IPR000459; --
INTERPRO; IPR003006; --
PFAM; PF00047; 1g; 3.
PROSITE; PS00290; IGMHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-80045036; Pubmed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1%; Score 834.5; DB 1
66.7%; Pred. No. 1.8e-60;
iive 34; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-1 CHAIN C REGION.
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CYTOPLASMIC
                            Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH1.
HINGE.
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Eukaryota; Metazoa; Chordata;
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223
327
362
398
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346
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398 AA;
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Matches 148; Conserv
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P01868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 124
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                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-85027161; Pubmed-6092053;
Mels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1963 constant region gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 842; DB 1; Length 333; 65.4%; Pred. No. 3.6e-61; live 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 SDGSFFMYSKLNVERSRWDSRAPFVCSVVHEGLHNHHVEKSISRPPGK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin domain; Immunoglobulin C region.
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                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89232738; Pubmed-3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM;
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PROSITE; PS00290; IG_MHC; 1.
  GAMMA-2B CHAIN C REGION.
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IG GAMMA-2B CHAIN C REGIC
Rattus norvegicus (Ràt).
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                                                                                                                                                                                                                              Gene 74:473-482(1988).
PIR; PS0018; PS0018.
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80
106
109
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106
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P03987;
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Length 398; Indels Page

between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDILINE-80012837; Pubmed=113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980). DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
Svasti J., Milstein C.;
The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972). CHAIN). CHAIN). CHAIN). INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN). "Evolution of immunoglobulin subclasses. Primary structure of region; Glycoprotein; Length 324; REMOVED POST-TRANSLATIONALLY -> D (IN REF. 3). -> D (IN REF. 3). A338812F3D1F2C93 CRC64; 65.1%; Score 822.5; DB 1; 60.9%; Pred. No. 1.3e-59; ive 45; Mismatches 37; N-LINKED (GLCNAC. PFAM; PF00047; iq; 3. PROSITE; PS00290; IG_MHC; 1. Immunoglobulin domain; Immunoglobulin C heavy chain."; Nucleic Acids Res. 6:3305-3321(1979) SEQUENCE (MYELOMA PROTEIN MOPC 21). MEDLINE=78242288; PubMed=98524; CH1. HINGE. murine myeloma gamma1 chain."; J. Biol. Chem. 253:6068-6075(1978) EMBL, V00793; CAA24172.1; -.
EMBL, V00793; CAA24173.1; -.
EMBL, V00793; CAA24174.1; -.
EMBL, V00793; CAA24175.1; -.
EMBL, V00795; CAA24176.1; -.
EMBL, V00795; CAA24176.1; -. Ψ. 35704 MGD; MGI:96446; Igh-4. INTERPRO; IPR000495; -. INTERPRO; IPR003006; -. 324 82 102 102 107 109 174 Alternative splicing 278 324 AA; 218 27 102 104 107 109 138 Adetugbo K.; CARBOHYD DISULFID DISULFID Query Match DISULFID DISULFID DISULFIL DISULFIL SEQUENCE NON_TER MOD_RES DOMAIN DOMAIN 

59 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 118 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 178 Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Rutheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus Gaps 2 PKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 59 60 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 11: 120 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 17 "Evolution of the rat immunoglobulin gamma heavy-chain gene family.", Gene 74:473-482(1988). 2 PKSCDKTHTCPPCPAPELLGG----PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 58 N-LINKED (GLCNAC. . .) (POTENTIAL). 013BAB45EF49B9DA CRC64; TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232 232 65.1%; Score 822.5; DB 1; Length 326; 61.5%; Pred. No. 1.3e-59; ive 43; Mismatches 38; Indels 9 CHAIN). CHAIN). CHAIN). region; Glycoprotein. INTERCHAIN (WITH A HEAVY CHAIN)
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INTERCHAIN (WITH A HEAVY CHAIN) PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) GAMMA-1 CHAIN C REGION. Immunoglobulin C CH1. HINGE. CH2. CH3. MEDLINE-89232738; PubMed=3149946; Brueggemann M.; MM; PFAM; PF00047; ig; 3. PROSITE; PS00290; IG_MHC; 1. 35946 Conservative STANDARD; INTERPRO; IPR000495; -. Immunoglobulin domain; 102 106 109 200 PIR; PS0017; PS0017 AA; Similarity SEQUENCE FROM N.A. Matches 144; DOMAIN DISULFID DISULFID DISULFID GC1_RAT P20759; DISULFID DISULFID DISULFID DISULFID SEQUENCE Query Match Best Local DOMAIN DOMAIN 180 66 66 g op δ q Q δ ð QQ ŏ g δλ qq δ

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MEDLINE-8222190; PubMed=6283537;
MEDLINE-8222190; PubMed=6283537;
MUCLECTURE-8222190; PubMed=628337;
MUCLECTURE-8222190; PubMed=8.

"Nuclectide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!-ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES BNCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED SEGMENT OF MU CHAINS.
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MEDLINE-82197626; PubMed-6604950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of immunoglopulin gamma chains.";
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
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EMBL; V00793; CAAZ4174.1; --
PIR; B02159; GIMSM.
MGD; MGI:96446; IGH-4.
INTERPRO; IPR000495; --
INTERPRO; IPR003006; --
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PROSITE; PS00290; IG_MHC; 1.
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Cell 18:559-568(1979).
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P01869;
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DOMAIN         1         97         CH1.           DOMAIN         98         110         HINGE.           DOMAIN         111         217         CH2.           DOMAIN         218         324         CH3.           DISULEID         102         INTERCHAIN (WITH A LIGHT CHAIN).           DISULEID         107         107         INTERCHAIN (WITH A HEAVY CHAIN).           DISULEID         109         INTERCHAIN (WITH A HEAVY CHAIN).           DISULEID         109         INTERCHAIN (WITH A HEAVY CHAIN).           DISULEID         138         198         N-LINKED (GLCNAC).           DISULEID         244         302         N-LINKED (GLCNAC).           DISULEID         244         357         POTENTIAL.           DOMAIN         358         393         CYTOPLASMIC (POTENTIAL).           SEQUENCE         393 AA, 43386 MM, 4CC88343B7AICE27 CRC64;         ACC64;	Local Similarity 60.8%; Score 817.5; DB 1; Length 398; Local Similarity 60.8%; Pred: No. 4.2e-59; Lilinininininininininininininininininini	13 C_RAT STANDARD: PRT; 329 AA. FEB-1991 (Rel. 17, Created) -FEB-1991 (Rel. 17, Last sequence update) -GAMMA-2C CHAIN C REGION. ttus norvegicus (Rat). tkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos manila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae DLINE-88166903; PubMed=3127222; Ueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.; equence of a rat immunoglobulin gamma 2c heavy chain constigution constigution with the constigution of a rat immunology to mouse gamma 3."; r. J. Immunol. 18:317-31911988). sayins-PROT entry is copyright: It is produced through a tween the Swiss Institute of Bioinformatics and the EBB e European Bioinformatics Institute. There are no restrict institutions as a long as its content in diffied and this statement is not removed. Usage by and titles requires a license agreement (See http://www.isb-sisend an email to licenseéisb-sib.ch).  BL; X07189; CAA30169-1; TERPRO; IPR000495; TERPRO; IPR000495; TERPRO; IPR000495; TERPRO; IPR000495; AM: PF00047; ig: 3 GSITE; PS00290; IG_MHC; 1.  Inmunoglobulin domain; Immunoglobulin C region. N_TER
FT DOD FT	Ouery Matches  Matches  QY 2  Db 99  QY 60  Db 152  QY 120  Db 212  Db 212  Db 272	SUL C

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EMBL; V00798; CAA24178.1; -.
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC;
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Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
                                                                                                                                                                                                                     VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 128
                                                                                                                                                                                                                                                  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence—mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                    PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                            Length 329;
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INTERCHAIN (WITH A HEAVY CHAIN)
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                                                                                                5FCD7B7933850773 CRC64;
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                                                                                                                                                 37;
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                                                                                                                            Score 809.5; DB 1
Pred. No. 1.5e-58;
; Mismatches 37
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-2A CHAIN C REGION, A ALLELE.
Mus musculus (Mouse).
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CH1.
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MEDLINE-74175517; PubMed=4831970;
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63.8%;
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329
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   Implications
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Rodentia; Sciurognathi; Muridae; Muringe; Mus
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immunoglobulin:amino-acid sequence of the Fc fragment. Implicator the evolution of immunoglobulin structure and function."; Eur. J. Biochem. 43:423-435(1974).
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de Preval C., Fougereau M.);
"Determination of the primary structure of a mouse gamma immunoglobulin. Identification of the disulfide bridges."
Eur. J. Biochem. 30:452-462(1972).
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 01, Last annotation update)
IG GAMMA-2A CHAIN C REGION, B ALLELE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertek
Mammalia; Eutheria; Rodentia; Sciurognathi; M
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                                                                                                                                                         MEDLINE=73056887; PubMed=4565406;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelib-sib.ch).
                                                                                                                                                                                                                                                                              Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; "Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.7%; Score 805; DB 1;
62.3%; Pred. No. 3.6e-58;
iive 38; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00479; -; NOT_ANNOTATED_CDS
MEDLINE=82037861; PubMed=6170065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.35
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02153; G2MSAB.
INTERPRO; IPR000495; -.
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                                                                                                                                                                                                                                                        SEQUENCE
    RAHARAK RAHARA
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185 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232 g δŏ

125 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 184

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Gaps

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48; Indels

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5 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV

Search completed: March 1, 2001, 09:17:41 Job time: 259 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 1, 2001, 09:13:22 ; Search time 79.26 Seconds
 (without alignments)
 198.750 Million cell updates/sec

US-09-389-782A-1 1263 1 EPKSCDKTHTCPPCPAPELL......MHEALHNHYTQKSLSLSPGK 232 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891

195891 seqs, 67900655 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:* Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Iq qamma-1 chain C		_	Iq qamma-1 chain C	-	Ig gamma-3 chain C	Ig gamma-3 chain C	Ig gamma-3 heavy c	Ig gamma-2 chain C	gamma-4		Iq qamma 2b chain	датта 2а		Ig gamma-2 chain C	Ig gamma 1 chain c	Ig gamma 3 chain c	Ig heavy chain pre		_		Iq qamma-2b chain	Ig gamma-3 chain C		Ig gamma-1 chain C			•	Ig gamma-2a chain
	ID	GHHU	869339	S72664	S31866	PT0207	A23511	. A60764	G3HUWI	G2HU	G4HU	GHRB	147160	147159	147162	G2GP	147158	147161	S22080	C30554	S31459	G3MSC	PS0018	G3MSM	PC4436	G1MS	PS0017	G1MSM	S00847	G2MSA
	DB	; 	7	7	4	7	7	~	-	H	٦	-	~	7	7	Н	7	~	~	~1	7	Н	7		7	П	ď	П	7	П
	Length	330	374	374	255	234	377	377	289	326	327	323	328	328	277	329	328	328	470	308	472	329	333	398	444	324	326	393	329	330
ap (	Watch	100.0	99.5	99.5	99.4	92.8	93.1	93.0	91.1	90.7	89.9	72.9	71.8	71.8	71.5	70.9	70.1	9.69	67.8	67.1	67.1	6.99	66.7	66.1	62.9	65.1	65.1	64.7	64.1	64.1
	Score	1263	1257	1257	1255	1210	1176	1174	1151	1145	1135	921	906.5	906.5	903	968	885.5	878.5	856		847.5	845.5	842	834.5	832.5	822.5	822.5	817.5	809.5	808
+[	No.	1	7	Э	4	Ŋ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A; Accession: A90564
A; Molecule type: protein
A; Residues: 136-154, Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E',
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
B; Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgGI-Immunglobulins (Myelomprotein

A,Molecule type: protein A;Residues: 1-96, R', 98-135 <CUN> A;Note: this sequence has the Glm(3) marker, 97-Arg R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M. Biochemistry 9, 3171-3181, 1970 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid A;Reference number: A90564; MUID:71064025

Ig gamma-2a chain Ig gamma-2a chain	19 gamma-za chain Ig gamma-za chain Ig gamma-za chain	Ig gamma-2b chain Ig gamma-2b chain	Ig gamma-2b chain Ig gamma-2 chain C	Ig gamma-2b chain Ig gamma heavy cha	Ig heavy chain vHI Ig heavy chain V-I	Ig gamma-1 chain C	Ig Y heavy chain (	Ig heavy chain pre
S37483 G2MSAB	S40295 PS0019	G2MS11 S25057	G2MSBM S06611	S01321 146732	S69340 A36040	S14236	B46529	S04845
777	100	7	7	2 2	2 2	7	~	~
335	446 322	336 474	405	475	249	152	572	549
64.1	62.9	61.7	61.3	60.1 56.0	45.7	45.2	31.3	28.8
809 805	794 785.5	779.5	774.5	759.5	577.5	571	395.5	364
30 31	333 4	35 36	37 38	39	41	43	44	45

## ALIGNMENTS

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RESULT 1	onno g gamma-1 chain C region – human C;Species: Homo sapiens (man)	C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Ju1-1999 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146	R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982	A:Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.	A;Reterence number: A93433; MUID:82274238 A;Accession: A93433	A; Molecule type: DNA A: Residues: 1-330 <fil></fil>	A. Cross-references: EMBL: 217370	A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker	Anote: 12s-350 is removed after translation R.Harris, 1. I	submitted to the EMBL Data Library, October 1992	A; Reference number: S33904	A; Accession: S36861	A; Molecule type: DNA	A; Kesidues: 2-330 (AAK)	A.C.U.S. TETETETETES. TEDELELIS V. R.Tatahashi, N.: Ueda S.: Obata M.: Nikaido, T.: Nakai. S.: Honio. T.	Cell 29, 671-679, 1982	A,Title: Structure of human immunoglobulin gamma genes: implications for evolution of	A. Reference number: S33887; MUID:83001943	A MACCESSION: 23200/	A; Residues: 88-113:235-330 <tak></tak>	A; Cross-references: EMBL: 217370	, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edel		A. P. C. Covalent Structure of a human gammaG-immunoglobulin. VII. Amino acid applications and the structure of a human gammaG-immunoglobulin. VII. Amino acid applications and the structure of a human gammaG-immunoglobulin.	A:Reletence unimer: A90:003; Mold://lookev24 A:Contents: mveloma proffein Fu	A, Accession: B90563	A. Moloculo tuno, nantotoin
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Gaps

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Eur. J. Blochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 < KMA>
A;Residues: 1-374 < KMA>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
$72664
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                143 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                               Score 1257; DB 2;
Pred. No. 2.9e-90;
2; Mismatches 0;
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99.1%; Pred. No. 2.9e-90;
ive 2; Mismatches 0;
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R; Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
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                                                                                                                                                                                                                                                                                               Query Match 99.5%;
Best Local Similarity 99.1%;
Matches 230; Conservative
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Matches 230; Conservative
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A; Accession: S72664
A; Status: preliminary
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                                                                                                        A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, 70, 36-96, 7K, 98-115, 70, 117-197, 7D, 199-238, 7D, 240, 7L, 242-268, 7E, 27
A; Note: 11-34, 70, 36-96, 7K, 98-115, 70, 117-197, 7D, 7, 198-3
A; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl KOI
A; Reference number: A91723; MUID:83289131
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
                                                                                                                                                                                                                                                                                                                                           A Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A: Molecule type: protein A: Molecule type: protein A: Molecule this sequence has the Glm(3) and Glm(non-1) markers B: Gall, W.E.; Edelman, G.M. B. Bidchemistry 9, 3188-3196, 1970 A: A: Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfic A: Reference number: A90565; MUD: 71064027 A: Contents: annotation; disulfide bonds B: Droker, L.; Schwarz, J.; Reichel, W.; Hllschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976 A: Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob A: Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob A: Reference number: A01667; MUID: 77070267 A: Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:120085; OMIM:147100
A; Map position: 14q32.33
A; Map position: 14q32.33-14q32.33
A; Introns: 99/1; 114/1; 224/1
C; Complex: An immunoqiobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamally: immunoqiobulin c region; immunoqiobulin c: region; immunoqiobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoqiobulin
F; 20-85/Domain: immunoglobulin homology < IMI>
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C;Accession: 563339
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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Pred. No. 8.4e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                     A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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C;Species: Homo saniene '---
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100.0%;
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Best Local Similarity 100.
Matches 232; Conservative
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Gaps

322

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Ig gamma-3 chain C region (allotype G3m(b)) - human C Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999 C;Accession: A23511 R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986 A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507 A;Accession: A23511 A;Accession: A23511 A;Residues: 1-377 CHUC> A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056 A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1;
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C; Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C; Accession: A60764
R; Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 256-257, 1989
A; Title: A human immunoglobulin ICHG3 allele (GmbO, bl, c3, c5, u) with an 1A; Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: immunoglobulin F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: immunoglobulin C region; immunoglobulin homology
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        190 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234
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Best Local Similarity 92.7%; Pred. No. 5.6e-84;
Matches 215; Conservative 8; Mismatches 9;
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A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 270/3
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Pred. No. 8e-84;
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20-85/Domain: immunoglobulin homology <IMM>
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F;20-85/Domain: immunoglobulin homology <IMM>
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92.78;
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Best Local Similarity
Matches 215; Conserv
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                                                                                                       Rifilpula, D.
Subnited to the EMBL Data Library, February 1993
A; Description: Screeing method for protein-protein interactions of cloned gene products.
A; Reference number: S31866
A; Accession: S31866
A; A; Accession: S31866
A; Molecule type: mRNA
A; Residues: 1-255 <FIL>
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C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, 2.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716
A;Accession: PT0207;
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                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
Kseywonds: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 ISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
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A; Residues: 1-234 <EHR>
C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin
E; 48-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1255; DB 4;
Pred. No. 2.5e-90;
0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 231; Conservative
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Best Local Similarity
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                                                                               C; Accession: S31866
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Best Local Simi
Matches 222;
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens
R; Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A; Reference number: A93906; MUD: 82197621
A; Recidues: 1.326 < ELL>
A; Ccoss-references: GB:V00554; GB:J00230; NID: 932759; PIDN: CABS8438.1; PID: 96066056
A; Notes: Lys-326 is probably removed posttranslationally
A; Residues: Lys-326 is probably removed posttranslationally
R; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J; Immunol. 125; 1048-1054, 1980
A; Title: The primary structure of a human IgC2 heavy chain: genetic, evolutionary, an A; Reference number: A92809; MUD: 81007873
A; Contents: myeloma protein Til
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 < WAN>
A; Residues: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.: Hofmann, T.
Can. J Biochem: 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains A; Reference number: M90752; MUD: 80001357
A; Contents: myeloma protein Zie
A; Accession: A90752; MUD: B0001357
A; Contents: myeloma protein Zie
A; Accession: A90752; MUD: A; Accession: A90752; MUD: A; Accession: A90752; MUD: A; Accession: A; Accession: A; Accession: A; Accession: A90752; MUD: A; Accession: A; Accession
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A; Molecule type: protein
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',
A; Note: this sequence has since been revised
B; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 933-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobul
A; Reference number: A93132; MUID:80114419
A; Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264-268
Ala and i
                                                                                                                                                                                                                                                                                                        59 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin
                                                                                                                                                                                                                                                            EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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A; Accession: By Protein
A; Residues: 238-275 <4067
A; Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation: Zie, revisions to residues 25, 59, 60, and A; Note: the revised sequence differs from that shown in having 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 231
                                                                                                                                                                        Indels
                                                                                    ; Score 1151; DB 1;
; Pred. No. 3.5e-82;
13; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-2 chain C region - human
                                                                                    91.1%;
90.5%;
                                                                                                                                                                        Conservative
                                                                                                                                Similarity
                                                                                                                                                                        209:
                                                                                    Query Match
Best Local S
Matches 209
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A.Residues: 1-289 <FRA>
A.Molecule type: protein
A.Residues: 1-289 <FRA>
A.Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A.Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cc
A.Note: the sequence of residues 42-76 was taken from the reference that follows
A.Note: the sequence of residues 42-76 was taken from the reference that follows
B. Franklin, E.C.
A.Note: the sequence of residues 42-76 was taken from the reference that follows
A.Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A.Reference number: A92219; MUID:77118561
A.Recession: A92219
A.Accession: A92219
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A; Accession: A93915
A; Accession: A93915
A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125, E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig gamma-3 heavy chain disease proteins - human C;Species: Homo sapiens (man) (c;Species: Homo sapiens (man) (c;Species: Homo sapiens (man) (c;Date: 31-Dec-1979 #sequence-revision 23-oct-1981 #text_change 16-Jul-1999 (c;Accession: A90442; A92219; A90198; A93915; A02149 (c;Accession: A90442; A92219; A90198; A93915; A02149 (c;Franklin, E.C. B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. A;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C. A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A;Reference number: A90442; MUID:81021548 (A)Contents: heavy chain disease protein Wis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: Protein
A; Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A; Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A; Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R; Wolfenstein-Todel, C; Franglone, B; Prelli, F; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A; Title: The amino acid sequence of "heavy chain disease" protein ZuC. Structure of the
A; Reference number: A90198; MUID: 77021516
A; Accession: A90199
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121 ISKAKGQPREPQYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                266 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 325
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A;Residues: 59-125, FBF, '128-226, 228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CHI region, an

R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E

Proc. Natl. Acad. Sci. U. S. A. 79, 3260-3364, 1982

A;Title: gamma heavy chain disease in man: cDNA sequence supports partial.

A;Reference number: A93915; MUID:82247835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
F; 203-270, Domain: immunoglobulin homology <IMM>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 6, 140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Gene: GDB:IGHG3
A)Cross-references: GDB:119339; OMIM:147120
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A; Molecule type: mRNA
A; Residues: 88-103, W, 105-143, E', 145-184, A', 186, E', 188-266 <MAR>
A; Residues: 88-103, W, 105-143, E', 145-184, A', 186, E', 188-266 <MAR>
A; Cross-references: GB:MI6426; NID:9165111; PIDN:AAA31289.1; PID:9165112
A; Note: this sequence has the dl1 allotyplic marker, 104-Met, and the e15 allotypic ma
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem J. 116, 249-259, 1970
Birtle: Sequence studies of the Rd section of the heavy chain of rabbit immunoglobul
A; Reference number: A90245; MUID:70110015
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A;Residues: 132-143, E', 145-161 <FRU>
K;Rill.I, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse
A;Reference number: A94416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Nucleotide sequence of a rabbit 1gG heavy chain from the recombinant F-I hap A,Reference number: A91749; MUID:84030930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabbit immunog
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A; Residues: 1-47, Ev. 49-71, FvV, 72-128 <PRA>
A; Rattens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy chain genes of rabbit 1gG; Isolation of a cDNA encoding gamma heavy
A; Reference number: A93928; MUID:83299917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marker,
                           C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20'85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Jonain: immunoglobulin homology <IM3>
F;240-307/Jonain: immunoglobulin homology <IM3>
F;140-307/Janidide bonds: interchain (to light chain) #status experimental F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
C;Eccession: K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 130
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A; Residues: 1-323 <BERA
A; Note: this sequence as the d12 allotypic marker, 104-Thr, and the e14 n
R; Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the Fd sections of rai
A; Reference number: A90290; MUID:76135469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
immunoglobulin C region; immunoglobulin homology plication; glycoprotein; heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                             Score 1135; DB 1; Length 327;
Pred. No. 7.1e-81;
8; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 LYSRLTYDKSRWQEGNVFSCSVMHEALHNYTQKSLSLSLGK 327
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.9%;
Best Local Similarity 93.7%;
Matches 208; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma chain C region - rabbit
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A; Map position: 14912.33-14932.33
A; introns: 99/1: 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-327 <ELL>
A; Note: the sequence was determined from the germline gene
R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           experimental
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C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
C;Rilison, J.; Buxbaum, J.; Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 ERKCCVE---CPPCPAPP-VAGPSVFLFPFKPKDTLMISKTPEVTCVVVDVSHEDPEVQF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 ISKTKGQPREPQVYTLPPSKEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;1470:sulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                       A; Contents: annotation; myeloma protein Sa, disulfide bonds R; Frangione, B.; Milstein, C.; Pink, J.R.L. Nature 221, 145-148, 1969
A; Title: Structural Studies of immunoglobulin G. A; Reference number: A93157; MID:69064124
A; Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1145; DB 1; Pred. No. 1.2e-81; Trans. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A90249; MUID:70207560
A;Accession: A90249
A; Reference number: A90253; MUID: 72033500
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A; Residues: 1-30; 81-326 <PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
A; Gene: GDB: IGHG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G4 HU
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Iggamma 2a chain constant region - pig (fragment)
Iggamma 2a chain constant region - pig (fragment)
C; Species: Sus scrofa domestice pig)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C; Accession: 147159
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences (A; Reference number: 147158; MUID:95015845
A; Accession: 147159
A; Constitution: 1
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Ig gamma 4 chain constant region - pig (fragment)
C;ppecies: Sus scrofa domestica (domestic pig)
C;pacies: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147162
R;Kacskovics, I:; Sun, J:; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Racskovics, II: Sun, J:; Butler, J.E.
A;Reference number: 147158; MUD:95015845
A;Recession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: II: 277 C;RACS
    71 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                               FFLYSKLFVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232 :||||| :|||| :||| :|||| :|||| XFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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Pred. No. 5.7e-63;
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72.1%;
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Matches 164; Conserv
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Best Local Similarity
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                                             225
                                                                                                                               189
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Q
                                    A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 129-131;155-172, 'D', 174-184,'A', 186,'E', 188-200,'D', 202-217,'E', 219-232,'Q',
A; Mote: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into la
C; Superfamily: immunoglobulin cregion; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E; 20-82/Domain: immunoglobulin homology <IMI>E; 30-92/Domain: immunoglobulin homology <IMI>E; 20-82/Domain: immunoglobulin homology <IMI>E; 2180-192/Domain: immunoglobulin homology <
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C;Species: Sus scrofa domestica (domestic pig)
C;Decies: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
R;Racskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3656.3573, 1994
A;Itle: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147188; MUID:95015845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.9%; Score 921; DB 1; Length 323; 67.3%; Pred. No. 2.8e-64; Live 31; Mismatches 34; Indels
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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A;Molecule type: MRNA
A;Molecule type: MRNA
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Matches 167; Conservative
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A Molecule type: protein
A) Residues: 227-311 <a href="mailto:creek">creek</a>
A) Residues: 227-311 <a href="mailto:creek">creek</a>
B) Coliveira, B): Lamm, M.E.
B) Coliveira, B): Lamm, M.E.
B) Contents an disulfide bridges of guinea pig gamma-2- immunoglobulin.
A) Freference number: A09354; MUID:71058474
A) Reference number: A09354; MUID:71058474
A) Rote: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
A) Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C) Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C) Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and isulfide bonds: In some cases, such as IgA and IgM, the subunits associate into Ia C) Superfamily: immunoglobulin immunoglobulin heterotetramer; immunoglobulin
E;21-81,00main: immunoglobulin homology cimi>
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A;Reference number: A90352; WUID:71058471
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A; Residues: 134-226 (TRA>
A; Residues: 134-226 (TRA>
B; Residues: 134-26 (TRA>
B; Residues: 134-881, 1974
B; Richemistry 13, 4804-4811, 1974
A; Title: Primary structure of the C-H3 homology region from guinea pig 1gG2 antibodies.
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A;Residues: 69-133:312-329 <TUR>
R;Tracey, D.E.; Cebra, J.J.
Blochemistry 13, 4795-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig 1gG2 antibodies.
A;Reference number: A90384; MUID:75036072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II.
A;Reference number: A90359; MUID:71058486
A;Accession: A90359
     <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
                                                    GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 125
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  Gaps
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29; Mismatches
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A; Residues: 1-3 «TRI»
Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Blochemistry 10, 18-25, 1971
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A; Accession: A90385
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A; Reference number: A94553
A; Accession: A94553
  Conservative
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A, Residues: 4-68 <BIR>
R; Turner, K.J.; Cebra, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A90384
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Matches 165;
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ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT 178
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F;28-79/Disulfide bonds: #status experimental
F;142-20/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental
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Best Local Similarity
Matches 164; Conserv
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March 1, 2001, 09:17:41 ; Search time 40.97 Seconds
    (without alignments)
316.083 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

US-09-389-782A-2 2179 1 MNKWLCCALLVLLDIIEWTT......QKLFLEMIGNQVQSVKISCL 401

Title: Perfect score: Sequence: Searched: 88757 segs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIE

		homo sapien	mus musculu	mus musculu		homo sapien		bos taurus	myxoma viru	variola vir	mus musculu	homo sapien	rattus norv	bos taurus	qallus qall	homo sapien	mus musculu	sus scrofa	homo sapien	sus scrofa	rattus norv	mus musculu	homo sapien	bos taurus	rattus norv	mus musculu	homo sapien	rattus norv	mus musculu	homo sapien	homo sapien	drosophila	homo sapien
	Description	2033	P25119	P27512	P25942	P36941	P25943	028203	P29825	P34015	P50284	P08138	P07174	P51867	P18519	P25445	P20334	077736	007011	P50555	P15725	P25118	P19438	019131	P22934	P47741	P43489	063199	P25446	P28908	P07942	P11046	P26842
S																																	
SUMMARIES	91	N.	TNR2_MOUSE	CD40_MOUSE	CD40_HUMAN	TNRC_HUMAN	VT2_SFVKA	CD40_BOVIN	VT2_MYXVL	VC22_VARV	TNRC_MOUSE	NGFR_HUMAN	NGFR_RAT	FASA_BOVIN	NGFR_CHICK	FASA_HUMAN	41BB_MOUSE	FASA_PIG	41BB_HUMAN	TNR1_PIG	OX40_RAT	TNR1_MOUSE	TNR1_HUMAN	TNR1_BOVIN	TNR1_RAT	OX40_MOUSE	OX40_HUMAN	FASA_RAT	FASA_MOUSE	CD30_HUMAN	LMB1_HUMAN	LMB1_DROME	CD27 HIMAN
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	P35556 homo sapien										Q93038 h wsl-1 pro
CD27_MOUSE	FBN2_HUMAN	LMG1_DROME	LMG1_HUMAN	LMA_DROME	PAC6_MOUSE	AGRI_CHICK	LMA1_MOUSE	LMA2_MOUSE	TSA4_GIALA	LMG1_MOUSE	WSL1_HUMAN
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# ALIGNMENTS

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RESULT	RESULT 1
D C	INR2_HUMAN STANDARD; PRT; 461 AA.
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DI	01-FEB-1991 (Rel. 17, Created)
i i	(Rel
- I	UI-OCI-2000 (Rel. 40, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE:	(D8d)
C C	INFRSFIB OR TNFRZ OR TNFBR.
SO	
ပ္ပ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
2 2	Mammalia; Eutheria; Frimates; Catarrhini; Hominidae; Homo.
Z (	[1]
구 :	SECUENCE FROM N.A.
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¥ :	Suitch C.A., Davis I., Anderson D., Solam L., Beckmann M.P., Jerzy K.,
X E	
Y 6	A leceptor to rumnor nectors ractor delines an unusual ramily of
7 6	CELILIAN AND VITAL PLOCETING. /
2 2	Science 240:1019-1023(1990).
Z (	
КР	SEQUENCE FROM N.A.
KX X	
КA	Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA	
RT	"A second tumor necrosis factor receptor gene product can shed a
RT	naturally occurring tumor necrosis factor inhibitor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96299745; PubMed=8661109;
RA	Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA	D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA	. X
E.	"Physical mapping and genomic structure of the human TNFR2 gene":
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7 0	JUNE OF A STATE OF THE STATE OF
4 4	ADDITION DOWN TO CONSTRUCT TO DESCRIPT DI PRANT D
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Z Z	Taiol Chem 265:1531-1536(1990)
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RX.	MEDLINE=91056048; PubMed=2173696;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING PORTION OF THERZ LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPPORS.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. DATABASE: NAME-PROW, NOTE-CD Guide CD120b entry;
DATABASE: NAME-Enbrel; NOTE-CD Guide CD120b entry;
DATABASE: NAME-Enbrel; NOTE-CLINICAL information on Enbrel;
WWW-"http://www.enbrelinfo.com/".
                                                                                                                                                                                                                                                                                                                                                                                                             Nature 398:533-538(1999).

-I-FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

-I-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
                                                                                                                   CHARACTERIZATION.
MEDLINE=93016040; PubMed=1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor.
Characterization of ligand binding, internalization, and receptor
Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX. MEDLINE-99221490; PubMed-10206649;
Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
"Structural basis for self-association and receptor recognition of
                                          of two
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                                  "Purification and partial amino acid sequence analysis of tw
distinct tumor necrosis factor receptors from HL60 cells.";
J. Biol. Chem. 265:20131-20138(1990).
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                                                                                                                                                                                                                                                phosphorylation.";
J. Biol. Chem. 267:21172-21178(1992)
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AAC50622.1;
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AAA36755.1;
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U52159; AAC50622.1;
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B35010.
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                     Brockhaus M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 ALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE=91187885; PubMed=1849278;
Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
"Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is species
specific.";
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01-MAY-1992 (Rel. 22, Created)
1-MAY-1992 (Rel. 22, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 314; DB 1; Length 46; Pred. No. 1.5e-15; 19; Mismatches 85; Indels
                                                                                                                                                                                                                                                                         BY SIMILARITY.
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N-LINKED (GLCNAC. ..) (POT
R -> P (IN REF. 4).
R -> M (IN R
       EXTRACELLULAR (POTENTIAL).
                                                                     CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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MEDLINE=91246168; PubMed=1645445;
Goodwin R.G., Anderson D., Jerzy R., Davi
Copeland N.G., Jenkins N.A., Smith C.A.;
                                       POTENTIAL.
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461 AA;
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                                                                                                                                Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
-!- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
'Molecular cloning and expression of the type 1 and type 2 murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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                                                                    Jacob C.O., Liu J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0652; TWFR.NGFR.1; 2.
PROSITE; PS50050; TWFR.NGFR.2; 3.
Receptor: Transmembrane; Glycoprotein; Repeat; Signal.
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TNFR-CYS 3.
TNFR-CYS 4.
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           receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
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EMBL; U39488; AAA85021.1; -.
EMBL; X87128; CAA60618.1; -.
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HSSP; P19438; 1NCF.
MGD; MGI:1314883; TNFRSF1B.
INTERPRO; IPR001368; -
                                                                                                         SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00020; INFR_c6; 4.
                                            SEQUENCE OF 1-26 FROM N.A.
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Matches 70;
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                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A., Howard M., Cockayne D.A.; "Genomic structure and chromosomal mapping of the murine CD40 gene."; J. Immunol. 149:3921-3926(1992).
110 GRYLEIEF-----CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIK 162
                  J. Immunol. 149:3921-3926(1992).

- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92105763; PubMed=1370315;
Torres R.M., Clark E.A.;
"Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation.";
J. Immunol. 148:620-626(1992).
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PROSITE; PS00620; TNFR_MGFR_1; 1.
PROSITE; PS00652; TNFR_NGFR_2; 4.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
SIGNAL 19 POTENTIAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). 4 X INFR-CYS.
                                                                                                                                                                                289 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE-93094586; PubMed-1281194;
                                                              163 HTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                  184 HRICS----ILAIPGNASTDAVCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M94126; AAA37404.1; --
EMBL; M94129; AAA37404.1; JOINED.
EMBL; M94128; AAA37404.1; JOINED.
EMBL; M94127; AAA37404.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M83312; AAB08705.1; -.
                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
215
289
187
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                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A46476; A46476.
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P25942; 1CDF
                                                                                                                                                                                                                                                                              TNFRSF5 OR CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Torres R.M.;
                                                                                                                                                                                CD40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS.
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                                                                                                                                                                                                                                                                                        SPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAGTPERNT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
CLOUD. RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
(TUMOR NECROSIS FACTOR RECEPTOR 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98266353; PubMed-9605317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Zheng Z., Naismith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
                                                                                                                                                                                                                                                                                                              84 EP--NQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVWEMATETIDI 141
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                    KYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC---VYC 83
                                                                                                                                                                                                                                                       30 QYLH-DGQ-----CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Construction and analysis of a detailed three-dimensional model of
the ligand binding domain of the human B cell receptor CD40.";
Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW: NOTE-CD guide CD40 entry:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 4.
ITNFR-CYS 4.
N-LINKED (GLCNAC. ..) (POTENTIAL).
C791CB6D2FEA574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-89356608; PubMed-2475341;
Stamenhovic I., Clark E.A., Seed B.;
A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";
EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein Sci. 7:1124-1135(1998).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
                                                                                                                                                Length 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                                                                                 142 VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                             141 VCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
                                                                                                                                              Score 270; DB 1; I
Pred. No. 1.2e-12;
5; Mismatches 68;
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3D-STRUCTURE MODELING OF 24-144.
                                                                                                                                                                                 26;
                                                                                            MM;
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                                                                                                                                              12.4%;
34.5%;
                                                                                          32111
                                                                                                                                                                                   Conservative
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103
144
187
153
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25
61
104
145
153
289 AA;
                                                                                                                                                                Similarity
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Best Local S
Matches 57
                                                       REPEAT
CARBOHYD
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---VYCSPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-COT-2000 (Rel. 40, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR)
LIBR OR INFCR OR INFRSF3.
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BC8776EC2C4A5680 CRC64;
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Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen
"Construction and evaluation of a hncDNA library of human 12p
transcribed sequences derived from a somatic cell hybrid.";
Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 TPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Indels
                                                                                                                     Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                      CD40L RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%; Score 261; DB 1; 33.9%; Pred. No. 5.1e-12; ive 23; Mismatches 74;
                                                                                                                                                                                                              TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
or send an email to license@isb-sib.ch)
                                                                                                                                                                               POTENTIAL.
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                                                                             PFAM; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 4.
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                     EMBL; X60592; CAA43045.1;
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                                                                   INTERPRO: IPR001368;
                                              PDB; 1CDF; 01-APR-97
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Eukaryota; Metazoa;
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111
125
153
180
277 AA;
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                                                                                                                     Receptor; B-cell;
                                                                                                                                3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LIVER;
                                    S04460;
                                                        MIM; 109535
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FUNCTION
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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9
                                                              FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 RDTVCATCAENSYNEHWNYLTICQLCRP-CDPVMGLEEIAPCTSKRKTQCRCQPGMFCAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 --LEIEFCLKHRSCPPGS-GVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 VLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQ--HRICCSRCPPGTYVSAKCSRI 75
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                                                                                -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                   Goodwin R.G., Smith C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93; Indels
                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                           LYMPHOTOXIN-BETA RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624626E6022F656F CRC64;
                                                                                                                                                                                                                                                        Receptor; Transmembrane; Glycoprotein; Repeat; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 244; DB 1; 26.9%; Pred. No. 1.4e-10;
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               MEDLINE=94225209; PubMed=8171323;
Crowe P.D., van Arsdale T.L., Walter B.N.,
Ehrenfels B., Browning J.L., Din W.S., Good
"A lymphotoxin-beta-specific receptor.";
Science 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
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PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
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MM:
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81
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168
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82
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PFAM; PF00020;
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Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
MCFadden G., Goodwin R.G.;
"T2 open reading frame from the Shope fibroma virus encodes a soluble
                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 QSVKQECNRTHNRVCECEEGRYLEIE-----FCLKHRSCPPGSGVVQAGTPERNTVCKK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 GHQ-----LLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKEL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GHDYEKDGLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR. 4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO
T
                                                                                                                                                                             Shope fibroma virus (strain Kasza) (SFV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                        seguence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem, Biophys, Res. Commun. 176:335-342(1991).
-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS IN REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.
                                                                    01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 30, Last annotation update)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                            MEDLINE-87321103; Pubmed-2820128;
Upton C., Delange A.M., McFadden G.;
"Tumorigenic poxviruses: genomic organization and DNA
telomeric region of the Shope fibroma virus genome.";
Virology 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (P
810530339198A71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%; Score 233.5; DB 1;
31.7%; Pred. No. 5.8e-10;
tive 19; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
     325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TWFR_NGFR_1; 2.
PROSITE; PS50050; TWFR_NGFR_2; 1.
Receptor; Glycoprotein; Repeat; Signal.
SIGNAL 1 16 POTENITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M17433; -; NOT_ANNOTATED_CDS.
EMBL; A23727; CAA01687.1; -.
                                            01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       llarity 31.7%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form of the TNF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00020; TNFR_C6; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
325
186
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104
147
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INTERPRO; IPR001368;
                                                                                                                                                                           Shope fibroma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
105
181
205
238
325 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                               Leporipoxvirus.
VT2_SFVKA
P25943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
CARBOHYD
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NREKYC 77

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CPPHTYSDSLSPTERCGTSFNYISVGFNLYPV-NETSCTTTAGHNEVIKTKEFTVTLNYT 207
                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                             CPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQKCGIDVTL---
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97281252; PubMed=9135560;
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (POTENTIAL)
. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P25942; LCC.
INTERPRO; IPR001368: -.
PFAM; PE00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
POTEWTIAL.
CD40L RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            746903F30F95F387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
                                                                                                                                                                                                           269 AA
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunology 90:294-300(1997)
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                TNFRSF5 OR CD40.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269
269 AA;
                                                                                                    202 -CEEAF 206
                                                                                                                                  208 DCDPVF 213
                                                                                                                                                                                                         CD40_BOVIN
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TRANSMEM
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SEQUENCE
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REPEAT
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                       134
                                             GTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQ 193
                                                          ---VYCSP-VCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQA 133
                                                                                                                                                                                                                                                                                                                                              tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR. 4 X TNPR-CYS. TNFR-CYS.
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L
                                                                                                                                                                                                                                                                         virinae;
                                                                                                                                                                                                                                                                                                                                                                                                                             REGION.
             TNF
                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                           PROBABLY PREVENTS
                                                                                                                                                                                                                                                           Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopox
                                                                                                                                                                                                                                                                                                                                                                            VITOLOGY 184:370-382(1991).
-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENT REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENT ANTIVIRAL EFFECTS OF THE CYTOKINE.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH
                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN
                                                                                                                                                                                                                                                                                                                     MEDLINE-91335768; PubMed-1651597; Upton C., Macen J.L., Schreiber M., McFadden G.; Maykona virus expresses a secreted protein with homology necrosis factor receptor gene family that contributes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABBF027E947292FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWER-CYS 2.

TWER-CYS 3.

TWER-CYS 4.

N-LINKED (GLCNAC...

N-LINKED (GLCNAC...
                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                                                                                            326 AA.
                                                                                                                                                                                                (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 38, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M95181; AAA46632.1; -.
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35208
                                                                                                                                                                              STANDARD;
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186
62
104
147
186
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181
205
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326 AA;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                          194 KCGIDVTL 201
                                                                                                                  195 LVVIPVTM 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
205
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27
27
63
105
148
66
                                                                                                                                                                                                                                                                                     Leporipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; A23729;
                                                                                                                                                                                                01-APR-1993 (
01-APR-1993 (
15-JUL-1999 (
                                                                                                                                                                           VT2_MYXVL
P29825;
                                                                                                                                                                                                                                                                                                                                                                     virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
CARBOHYD
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81
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DB 1; Length 326;

10.1%; Score 220;

Query Match

5;

Gaps

18;

89;

; Score 228; DB 1; ; Pred. No. 1.1e-09; 21; Mismatches 89;

10.5%;

Similarity 31.9%

:09

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Query Match Best Local S. Matches 60

Length 269; Indels 29 LHYDPETG-----HQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC 80

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                        ů,
                                                                                                                                                                                                                                                                                                                                                                                                   RTHNRVCECEEGRYLEIE-----FCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSG 152
                                                                                                        211
                        Gaps
                                             LLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECN 98
                                                                     97
                                                                                                                                                                                                                                                                                                                                                        Variola virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                        157 AVSSTETC----TSSFNYISVEFNLYPVNDTSCTTTAGPNEVVKTSEFSVTLNHTDCDP
                                                                  LCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCD
                                                                                                                                        ETSSKAPCIKHTNCSTFGLLLIQKG - - - - NATHDNVCSGNREATQKCGIDVTL - - - - CEE
                       20;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR-CYS 1.
TNFR-CYS 2.
D45D40B5C6E780EF CRC64;
5.4e-09;
                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
PROTEIN C22/B28 HOMOLOG.
                                                                                                                                                                                                                                                                          349 AA.
            Pred. No. 5.4e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 X TNFR-CYS.
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00020; TNFR_C6; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                      24; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TN
108
38189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X69198; CAA49137.1; -.
EMBL; X67117; CAA47540.1; -.
PIR; D36858; D36858.
PIR; S35987; S35987.
PIR; S46888; S46888.
HSSP; P19438; 1NCF.
           29.1%;
                      Conservative
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR001368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
31
67
349 AA;
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                Orthopoxvirus.
                                                                                                                                                                                                               213
                                                                                                                                                                                       205 AF 206
                                                                                                                                                                                                                                                                       VC22_VARV
P34015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
            Local
                                                                                                                                                                                                               212 VF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                            39
                                                                  38
                                                                                          66
                                                                                                                                        153
                                                                                                                                                                                                                                                           VC22_VARV
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                            66 TPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCK 125
                                                                                                                                                                                                                                                             ---TITMNHTDCNPVFREEYFSVLNKVATSGFFTGENRYQNISK-----VCTLNFEIK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Browning J.L., Ware C.F.;
"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Honjo T.;
"The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping.";
Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVERIKRRHSS-----QEQTFQLLK-----LWKHQNRDQEMVKKIIQDIDLCESSVQRH
11 FLSCIIINGRDAAPYT----PPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQC
                                                                                                                                                                                                                 117 FCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ-
                                                                                                                                                                                                                                                                                                                                                           176 KGNATHDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 LGHSNLTTEQLLALMESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                              184 TLYPVNDTSCT----RTTTTGLSE-------SILTSEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                   63 VPCPDHSYTDSWHISDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CVB; TISSUE-LUNG;
MEDLINE-96072804; PubMed-7594541;
Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 -- YRVGNVLDDDSHMPGSCNIHKPITNS-- KPTRFL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 LMYALKHL--KTSHFP-----KTVTHSLRKTMRFL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 155:5280-5288(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U29173; AAA68964.1; -. EMBL; L38423; AAB00846.1; -. EMBL; U30798; AAA81334.1; -. HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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17;

84;

10.0%; Score 217; DB 1; Length 349; 23.2%; Pred. No. 9.6e-09;

51; Mismatches 169; Indels

92; Conservative

Matches

δλ

Local Similarity

Query Match

4 WLCCALLVLLDIIEWTTQETLPPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLC

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             LLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
SIMILARITY: CONTAINS A LA-NGFR/TNFF-TYPE CYSTEINE-RICH REGION.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TWFR_NGFR_1; 3.
PROSITE; PS50050; TWFR_NGFR_2; 4.
PROSITE; PS50017; DEATH_DOMAIN;
PROSITE; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (P. B09FA143FB3D625B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 199; DB 1;
Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEATH DOMAIN.
BY SIMILARITY.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                                                                                                                                                                                                                                              EMBL; M14764; AAB59544.1; -. EMBL; M21621; AAA36363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO, IPRO00488; -.
INTERPRO, IPR001368; -.
PFAM; PF00020; INFR_c6; 4.
PFAM; PF00531; death; 1.
SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                           PIR; A25218; GOHUN.
HSSP; P07174; 1NGR.
MIM; 162010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
52; Conserv
                                                                                                                                               BOND FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation;
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEIE--FCLKHR--SCPPGS-GVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----HYDPETGHQLLCDKCAPGTYLKQHCTVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A. MEDINE-87051725; Pubmed-3022937; Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E., Bothwell M., Chao M.;
                                                                                                                                                                    4 X TWER-CYS.

TWER-CYS 1.

TWER-CYS 3.

TWER-CYS 3.

TWER-CYS 4.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Last sequence update)
1-COT-2000 (Rel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
(GP80-LNGFR) (F75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94; Indels
                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                           LYMPHOTOXIN-BETA RECEPTOR
                                                                            Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         29B326A566AEF661 CRC64;
                                                                                                                                          POTENTIAL. CYTOPLASMIC (POTENTIAL).
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Eukaryota; Metazos; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Expression and structure of the human NGF receptor. Cell 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 206; DB 1;
Pred. No. 7.2e-08;
; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Scur
26.1%; Pred
32;
             INTERPRO; IPR001368; -. PFAM; PF00020; TNFR_C6; 3. PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LLVLLDIIEWTTQETLPPKYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            44956 MW;
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   MGD; MGI:104875; LTBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           415 AA;
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                                                                                                                                                                                                                                                                                                                    101
104
126
139
142
172
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59
62
83
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P08138;
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                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
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9

Gaps

16;

71; Indels Length 4

(POTENTIAL)

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E S E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.; "NMR structure of the death domain of the p75 neurotrophin receptor."; EMBO J. 16:4999-5005(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93077038; PubMed-1446821;
Metsis M., Timmusk T., Allikmets R., Saarma M., Persson H.;
"Regulatory elements and transcriptional regulation by testosterone
and retinoic acid of the rat nerve growth factor receptor promoter.";
Gene 121:247-254(1992).
           -SYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLE----IEFCLKHR 122
                                   71 VTFSDVVSATEPCKPCTE-CVGLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEAC---R 126
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                         L.A., Shooter E.M.; rat nerve growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: N - AND O-GLYCOSYLARED AND IS PHOSPHORYLAPED ON SERINE.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                       01-APR-1988 (Rel. 07, Created)
1-APR-1988 (Rel. 07, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : - FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF,
                                                                              127 VCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVC 170
                                                                SCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNC 166
                                                                                                                                                                                                                                                                                                                                                          Radeke M.J., Misko T.P., Hsu C., Herzenberg "Gene transfer and molecular cloning of the
                                                                                                                                                             425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LA A01269; -; NOT_ANNOTATED_CDS.
PIR; A26431; A26431.
PDB; LNGR; 29-JUL-97.
INTERPRO; IPRO00488; -.
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00652; TNFR_NGFR_1; 3. PS50050; TNFR_NGFR_2; 4. PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-87115859; PubMed-3027580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97449145; PubMed=9305641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 334-418,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00020; TNFR_c6; 4. PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                Nature 325:593-597(1987)
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                           norvegicus (Rat).
                                                                                                                                                                                                                                               GP80-LNGFR) (P75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=LIVER; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
                                                                                                                                                             NGFR_RAT
P07174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                   receptor
                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                  RESULT 12
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347 EVEKLLNGDTWRHLAGELGYQPEHIDSFTHEAC----PVRALLASW----GAQDSATLA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTFSDVVSATEPCKPCTE-CLGLQSMSAPCVEADDAVCRCAYGYYQDEETGHCEACSVFE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :: | : | | : | | : VITVMG-----SSOPVVTRGTTDNLIPVYCSILAAVVVGLVAYIAFKRWNSCKONKQGA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVKKIIQ-----LMESLPGKKF- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 NSRPVNQTPPPEGEKLHSDSGISVDSQSLHDQQTHTQTASGQALKGDGNLYSSLPLTKRE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIE--FCLKHRSCP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AVPTK--IIPNWLSYL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDSLPGTKVNAESVERIKRRHSSQE-------QTFQLLKLWK--HQNRDQE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ISPEEIER-TRKTCKSSEQLLKLLSLWRIKNGDQD--TLKG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLILGVSSGGAKETCSTGLYTHSGE-----CCKACNLGEGVAQPCGA-NQTVCEPCLDN 71
                                                                                                                                                                                                   BY SIMILARITY.

N-LINED (GLCNAC. ..) (POTENTIAL).

N-LINED (GLCNAC. ..) (POTENTIAL).

N-LINED (GLCNAC. ..) (POTENTIAL).
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                          LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3e-07
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                                                                                                                            TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 197.5;
Pred. No. 3e
                                                                                                  TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
                                                                                                                  INFR-CYS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGNREATQKCGIDVTLCEEAFFRF------
Signal; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FASA_BOVIN STANDARD; P51867; 01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      45432 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: ||: ::
399 LLAALRRIQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                    425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMYALKHLK 353
Phosphorylation;
                                                                                                  32
32
67
67
109
149
198
33
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                                                                      FRANSMEM
DOMAIN
                                                                                                                                                                                                         DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                REPEAT
REPEAT
                                                        DOMAIN
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                                                                                                                   RPEAT
                                                                                                                                                               REPEAT
                                                                                                                                                                                             DOMAIN
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                            CHAIN
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19;

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149 FFSGETSSKAPCIKHINCSTFGLLLI--
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
261
416
181
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
262
263
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=BRAIN;
                                                                                                                                                                                                                               NGFR_CHICK
P18519;
                                                                                                                                             293 E 293
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TRANSMEM
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DOMAIN
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                                                                                                                                                                    318
                                                                                                                                                                                                                   CHICK
                         164
                                                                                                                     g
                                                                                                                                                                    qq
                       g
                                               δ
                                                                       qq
                                                                                               Qγ
                                                                                                                                              δλ
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                             MEDLINE=96226401; PubMed=8634151;

A Yoo J., Stone R.T., Beattie C.W.;

Toloning and characterization of the bovine Fas.";

DNA Cell Biol. 15:227-234(1996).

-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE BADATOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEOLYTING APOPTOSIS. FAS-WEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STHULATED

SIGILDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGS----GVVQAGTPERNTVCKKCPDG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HQLLCDKCAPGTYLKQHCTVRRKT-LCVPCPD-HSYTDSWHTSDECVYCSPVCKELQ--S 92
                                                                                                                                                                                                                                                                                                    DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50005; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4D88A90E9E1F4892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9e-07;
es 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
8.7%; Score 190.5;
Best Local Similarity 25.6%; Pred. No. 6.9e
Matches 77; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
FASL RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEATH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFR-CYS 2. TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U34794; AAC48546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00020; INFR_c6; 3. PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36445
                                (APO-1 ANTIGEN) (CD95).
TNFRSF6 OR APT1 OR FAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPR000488; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                               Bovidae; Bovinae; Bos.
                                                            Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA;
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P25445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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-- OKGNATHD -- NVCSGNREAT 192
                                                                                                                                                                                         257
                                                                                                                                                                                                                                                    292
                                                                                                                                                                                                                                                                                        | : | | | | | | : : : | : : | | : : | | 258 NVHETAEQKVQLLRNWYQSHGKKNAYCTLIKKSLPKALAEKICDIVMKDITNERENANLQN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
LOW AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
(GP80-LNGFR) (P75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P., Shooter E.M., Reichardt L.F.; Shooter E.M., Reichardt E.F.; Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system."; Neuron 2:1123-1134(1989).
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-!- SIMILARITY: CONTAINS A LA-NGFR/TWFR-TYPE CYSTEINE-RICH REGION.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                          ---GSRS------HAN-SLWALLILLIPIVLIIYKVVKSRERNKKNDYCNSAASNDEGR
                                                                                                                                                                                                                                                    242 RRHSSQEQTFQLLKLW--KHQNRD-----QEMVKKIIQDI-DLCESSVQRHLGHSNLTT
                                                                                                                                                                                      213 QLNLTDVDL-----GKYIPS----IAEQMRITEVKEFVRKNGMEEAKIDDIMHD
                                                                                                                        193 QKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTK----VNAESVERIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
LOW-AFFINITY NERVE GROWTH FACTOR
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PIR; A60504; A60504.

HINTERPRO; IPR001488; -

INTERPRO; IPR001368; -

PFAM; PF00020; TNFR_GE; 4.

PROSITE; PS0052; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 3.

PROSITE; PS50050; TNFR_NGFR_2; 3.

PROSITE; PS50010; DEATH DOMAIN; 1.

Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 CDKCAPGTYLKQHCTVRRKTLCVPCPDH-SYTDSWHTSDECVYCSPVCKELQSVKQECNR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 CKACNLGEGVVQPCGV-NQTVCEPCLDSVTYSDTVSATEPCKPCTQ-CVGLHSMSAPCVE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91309137; PubMed=1713127;
Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
Sameshima M., Hase A., Seto Y., Nagata S.;
"The polypeptide encoded by the CDNA for human cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen.";
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01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
(APO-1 ANTIGEN) (CD95 ANTIGEN)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335. MEDLINE-92268122; PubMed-1375228; Ochm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C., Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
                                                                                                                                                                                                                                                                                                                                                                                                                 .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 8.4%; Score 184; DB 1; Length 416; Local Similarity 30.9%; Pred. No. 2.7e-06; les 46; Conservative 28; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6BCEAAB54F4D2D56 CRC64;
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                                                                                                                                                                                SIMILARITY.
                                                                                                                DEATH DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
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                                                                                                                                                                                                                                                                                                                      BY SIMILAN
BY SIMILAN
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BY SIMILAN
N-LINKED
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Cell 66:233-243(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AA;
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P25445;
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DISULFID
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                  STRUCTURE BY NMR OF 218-335.
MEDLINE-97122332; PubMed-8967952;
Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
"NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
Nature 384:638-641(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDECVYCSPVCKELQSVKQE--CNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 TTVETQNLEGLHHDGQFCHK----PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHF 97
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TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 2.
TNER-CYS 3.
DEATH DOMAIN.
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                          -! - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 182; DB 1; Length 335; ilarity 25.5%; Pred. No. 2.9e-06; Conservative 34; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FASL RECEPTOR.
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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J. Biol. Chem. 267:10709-10715(1992).
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PIR; S24543; S24543
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Best Local Similarity
Matches 76; Conserv
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198 -----TCRKHRKENQGSHESPTLNPE----TVAINLSDVDLSKYITTIAGVMTLSQVK 246
135 TPERNTVCKKCPDGFFSGET-SSKAPCIKHTNCSTFG----LLL------IOKG 177
               178 NATHDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTK----- 231
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Search completed: March 1, 2001, 09:17:44 Job time: 262 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

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343.530 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-389-782A-2 2179 1 MNKWLCCALLVLLDIIEWTT......QKLFLEMIGNQVQSVKISCL 401

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 Total number of hits satisfying chosen parameters:

195891 seqs, 67900655 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qene murine tumour	tumor necrosis fac	tumor necrosis fac	B cell-associated	B cell-associated	B-cell activation	tumor necrosis fac	T2 protein - rabbi	T2 protein - myxom	gene G4R protein -	G2R protein - vari	hypothetical prote			nerve growth facto	apoptosis-mediatin	FAS soluble protei	T-cell antigen 4-1	4-1BB - human	lymphocyte activat	tumor necrosis fac	OX40 antigen precu	S	tumor necrosis fac	tumor necrosis fac	tumor necrosis fac	gene ox40 protein	OX40 homolog - hum	Fas antigen precur
SUMMARIES	ID	88	A35356	B38634	A46515	A46476	A60771	154182	B43692	GQVZML	D36858	D72175	T28623	COHON	A26431	JN0006	A40036	137383	B32393	I38426	JT0752	JC4302	S12783	GQMST1	157826	GQHUT1	GQRTT1	148700	137552	JC2395
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	Match Length	4	461	474	289	305	277	435	325	326	349	349	348	427	425	416	332	314	256	255	255	461	271	454	454	455	461	272	277	324
8. Outerv	Match	14.4	14.3	14.3	12.4	12.4	12.0	11.2	10.7	10.1	10.0	6.6	6.6	9.1	9.1	8.4	8.4	8.2	8.1	7.7	7.6	7.6	7.5	7.4	•	7.3	٠	•	6.9	6.8
	Score	314	312	312	270	270	261	244	233.5	220	217	216	215.5	199	197.5	184	æ	179.5	177	167	166	165.5	163	161.5	161.5	160	153	152.5	151	147.5
Result	NO.	-4	7	e	4	5	9	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	. 52	26	27	28	29

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apoptosis-mediatin hypothetical prote laminin alpha chai CD30 antigen precu subtilisin-like pr subtilisin-like pr laminin beta-1 cha CD27 antigen precu cocyst wall protei laminin beta-1 cha socyst wall protei laminin beta-1 cha serine proteinase furin (EC 3.4.21.7 hypothetical prote CD27 antigen precu fibrillin-2 precu		rotein - mouse (fragment) 996 #text_change 23-Jul-1999 odd, J.A. necrosis factor receptor gene. DDBJ	CAA53981.1; PID:9433831 2; NGF receptor repeat Domo > Length 459;	hes 79; Indels 26; Gaps 4; -OLLCDKCAPGTYLKQHCTYRKTLC 62  :	AVCECEGRYLEIEF 117	SKAPCIKHTNCSTFGLLLIQ 175	
2 A46484 2 T23064 2 T43291 2 A42086 2 G00428 1 WMHUBI 1 A46517 2 A44456 1 MMFFBI 2 S36016 1 MMFFBI 2 A34583 2 T25933 1 A49053 2 A54105	ALIGNMENTS	use) ision 02-Jul-1 erson, L.B.; T type 2 tumor 95178848	NID:9433830; tor receptor peat homology Score 314; Pred. No. 1.	20; Mismatc	VPCPDHSYIDSWHISDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIEF	CLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ  ::         :      :	
6.6 6.5 6.5 8.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 6.3 102 7 102 7 102 7 102 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 102 7 102 7 102 7 102 7 102 7 102 7 102 7 102 102 102 102 102 102 102 102 102 102		necrc ulus #sec ker, -727, -727, riati	1.439 < KES> erences: EMBL:X76401; NID: 1y: tumor necrosis factor omain: NGF receptor repeat ch 1 Similarity 34.6%; Pre	Conservative PPKYLHYDPETGH   :        : PAQVVLTPYKPEPGY	IDSWHISDECV)    :  :  QVWNQFRICL	CPPGSGVVQAG:         : CGPGFGVASSR	VCS 186
143 142.5 142.5 142.5 137.5 137.5 137.5 128.5 128.5 128.5 126.5 125.1 125.1		tum Mus Jul- Jul- : I4 e 5, e 5, e 5, reli	1-4 eren 1y: omai ch ch		63 VPCPDHSY       62 ADCEASMY	18 22 RQ	176 KGNATHDNVCS
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1148854 148854 G.Species: 05. C.Date: 02. C.Accession R.F.Powell, E Mamn. Genom A.Title: All A.Reference A.Reference A.Accession A.Status: p	Cro Sup 151 151	Matches Qy 18 Db 2	Qy Db	Qy 1 Db 1	0y 1

178 PGNASTDAVCA 188

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tumor necrosis factor receptor type 2 precursor - human N;Alternate names: 75K tumor necrosis factor receptor

C; Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35356; A36475; A48416; A36007; A33666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular a A;Reference number: A35356; MUID:90260639

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50 LKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEE 109
     F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TFGLLLIQKGNATHDNVCS 186
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187 VVAI----PGNASMDAVCT 201
                                                                                                                                                             14.38;
34.78;
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Matches 70; Conserv
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                                                                                                                                                                                                                                                                    69;
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Best Local &
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A; Residues: 23-461 CDEM>
A; Residues: 23-461 CDEM>
A; Residues: 23-461 CDEM>
A; Cross-references: GB:563368; NID:9235648; PIDN:AAB19824.1; PID:9235649
A; Cross-references: GB:563368; NID:9235649; NID:9235649
A; Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
B; Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
A; Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A; Reference number: A36007; MUID:90349572
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A; Residues: 116-140, P',142-195, R',197-362, T',364-461 <HEL>
A; Residues: 116-140, P',142-195, R',197-362, T',364-461 <HEL>
A; Cross-references: GB:MASS87; NID:G339751; PIDN:AAA63262.1; PID:G339752
R; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
J. Hille: Purification and partial amino acid sequence analysis of two distinct tumor ned
A; Reference number: A23666; MUID:91056048
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Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934
                                                                                                                            A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-195, R', 197-461 < KOH>
A; Residues: 1-195, R', 197-461 < KOH>
A; Createneres: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
A; Demblc, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A; Reference number: A48416; MUID:91370690
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A;Molecule type: protein
B;Engelmann, H.; Novick, D.; Wallach, D.
B;Engelmann, H.; Novick, D.; Wallach, D.
A;Engelmann, H.; Novick, D.; Wallach, D.
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
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Aintrons: 26/3
Aintrons: 26/3
Aintrons: 26/3
Aintrons: 26/3
Aintrons is incomplete
Aintrons is incomplete
Cisuperfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
Cisuperfamily: tumor necrosis factor receptor; transmembrane protein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor type 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NGI>
F;78-119/Domain: NGF receptor repeat homology <NGI
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F;280-461/Domain: intracellular #status predicted <INT>
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Molecule type: protein
Residues: 27-31 <ENG>
                                                                                                            A; Residues: 1-461 <SMI>
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Residues: 1-37 <RES>
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preliminary
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A, Molecule type: mRNA
A, Residues: 1-474 < Libb.
A, Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828
A; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A; Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A; Reference number: A40254; MUID: 91246168
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A; Residues: 1-474 <600-
A; Cross-references: GB: M60469; NID: 9199827; PIDN: AAA39752.1; PID: 9199828
A; Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
Submitted to the EMBL Data Library, May 1995
A; Description: Characterization of the promoter region of the murine p75-TNF receptor
A; Reference number: S54816
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(5)Species: Mus musculus (house mouse)
(c)Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
(5)Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Arritle: Gloning and expression of cDMAs for two distinct murine tumor necrosis
A; Reference number: A38634; MUID:91187885
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-22 <KIS>
A; Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044
C; Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homolo
C; Keywords: cytokine receptor; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>F; 23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>F; 40-77/Domain: NGF receptor repeat homology <NG1>F; 79-120/Domain: NGF receptor repeat homology <NG2>F; 166-203/Domain: NGF receptor repeat homology <NG3>F; 166-203/Domain: NGF receptor repeat homology <NG3>F; 166-203/Domain: NGF receptor repeat homology <NG3>F; 166-203/Domain: NGF receptor repeat homology <NG4>F; 166-203/Domain: NGF receptor repeat homology <NG5-F; 166-203/Domain: NG5-F; 166-203/Domain: NG5-F; 166-
                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 CTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 EI-----EFCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCS 167
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 9 ALAVGLEL--WAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --QLLCDKCAPGTY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LWVALVFELQL - WATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQY 63
                                                                                                                                                                                                                                                                                             8 ALLVLLDIIEWTTQETLPPK--YLHYDPETGH------QLLCDKCAPGTYLKQH 53
                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 474;
Score 312; DB 1; Length 46
Pred. No. 2.4e-14;
Or Wismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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llarity 34.3%; Pred. No. 2.4e-14;
Conservative 22; Mismatches 84.
                                                                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LCCALLVLLDIIEWTTQETLPPKYL--HYDPETGH-
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antigen; transmembrane prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1.277 **CSTA>
A; Cross-references: EMBL: X60592; NID: 929850; PIDN: CAA43045.1; PID: 929851
R; Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann,
J. Immunol. 142, 562-567, 1989
A; Title: Biochemical characteristics and partial amino acid sequence of the recept
A; Reference number: A60771; MUID: 89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: GDB:215268; OMIM:109535
A.Map position: 20q12-20q13.2
C.Superfamily: CD27 antigon; NGF receptor repeat homology
C.Keywords: B-cell; glycoprotein; phosphoprotein; surface antigon; transmemk
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>F;21-193/Domain: extracellular #status predicted <EXT>F:21-15/Domain: transmembrane #status predicted <TMM>F;194-215/Domain: intracellular #status predicted <CYT>F:194-217/Domain: intracellular #status predicted <CYT>F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Homo sapiens (man)
Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 SPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAGTPERNT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VYCSPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAG 134
                                                                                                                                                                                                                                                                                                                                84 EP--NQELRVKKEGTAESDIVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETIDI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                           30 QYLH-DGQ-----CCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          KYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC---VYC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHYDPETG------HQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPERNIVCKKCPDGFFSGETSSKAPCIKHINCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|:|: || |||| :|: | | || || TGVSDTICEPCPVGFFSNVSAFEKCHPWTSCETKDLVVQQAGTNKTDVVC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nerve
                                                           305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 277;
                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                       141 VCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 261; DB 2; I
Pred. No. 4.6e-11;
3; Mismatches 74;
                                                        Score 270; DB 2;
Pred. No. 1.2e-11;
; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Stamenkovic, I.; Clark, E.A.; Seed, B.
Brbo J. 8, 1403-1410, 1989
A;Title: A b-ymphocyte activation molecule related
A;Reference number: S04460; WUID:89356608
A;Accession: S04460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-cell activation protein CD40 precursor - human N;Alternate names: B-cell surface antigen Bp50
                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%; Scillarity 33.9%; Pro
Conservative 23;
                                                        12.4%;
llarity 34.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S04460; A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 21-50 < BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A60771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                 57;
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Best Local S:
Matches 58
                                                        Query Match
Best Local
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                                                                                                                 Matches
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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
R:Totas: Calark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A:Reference number: A46476
A:Residues: 1-305 <-TOR>
A:Residues: 1-305 <-TOR>
A:Residues: 1-305 <-TOR>
A:Residues: 1-305 <-TOR>
A:Residues: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A:Note: sequence extracted from NCBI backbone (ABBAN entry MUSCD40A, release 113.0
C:Comment: For an alternative splice form, see PIR:A46515
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Reywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <-NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.A.; Howard, M.; Cockayne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 26-May-2000
124 GRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPVCKELQSVKQECNRTHNRVCECEEGRYL---EIEFCLKHRSCPPGSGVVQAGTPERNT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping of the murine CD40 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                       B cell-associated surface molecule CD40, short splice form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell-associated surface molecule CD40, long splice form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-289 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A) Experimental Source: BALB/C, liver
A) Note: sequence extracted from NCBI backbone (NCBIP:120357)
C) Comment: For an alternative splice form, see PIR:A46476
C) Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: alternative splicing
F;105-144/Domain: NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.; Clark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 VCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.4%; Score 270; DB 2; 34.5%; Pred. No. 1.2e-11; tive 26; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994
C;Accession: A46515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rigrimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, J. Immunol. 149, 3921-3926, 1992
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping A;Refere number: A46515; MUID:93094586
A;Accession: A46515
                                                                                                                                                                                               163 HTNCSTFGLLLIQKGNATHDNVCS 186
                                                                                                                                                                                                                                   Similarity 34.5
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 57;
                          64
                                                                                110
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C;Species: variola virus
C;Decies: variola virus
C;Decies: variola virus
C;Decies: variola virus
C;Decies: variola virus
C;Decession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Description: not shown.
A;Reference number: A36859
A;Reference number: A36858
A;Status: preliminary
A;Residues: 1-349
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Residues: 1-349
A;Cross-references: GB:X69198; NID:g456758; PiDN:CAA49137.1; PID:g457087
A;Cross-references: GB:X69198*
A;Cross-references: GB:X69198*
A;Cross-references: GB:X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cippecies: myxoma virus (strum because)
Cippecies: myxoma virus
Cippecies: myxoma virus
Cipate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-199
Cipate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jun-1991
Cipate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jun-1992
Cipate: 31-Dec-1992 #text_change 19-Dec-1992 #text_change 19-Jun-1992
Cipate: 31-Dec-1992 #text_change 19-Dec-1992 #text_change 19-Dec-1992
Cipate: 31-Dec-1992 #text_change 19-Dec-1992
Cipate: 31-Dec-1992
Cip
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C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession: D36858; S46888; S32385; S35987
90 LSESQPCDRTHDRVCNCSTGNYCLLKGQNGCRICAPQTKCPAGYG-VSGHTRAGDTLCEK 148
                                                                                                                                                               149 CPPHTYSDSLSPTERCGISFNYISVGFNLYPV-NETSCITTAGHNEVIKTKEFTVILNYT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIHNRVCECEEGRYLEIE-----FCLKHRSCPPGSGVVQAGTPERNIVCKKCPDGFFSG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 LCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKQECN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTDCDP
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                                                                                        145 CPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQKCGIDVTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 ETSSKAPCIKHTNCSTFGLLLIQKG----NATHDNVCSGNREATQKCGIDVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 220; DB 1; L 29.1%; Pred. No. 3.8e-08; ive 24; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein - myxoma virus (strain Lausanne)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qene G4R protein - variola virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 29.153; Conservative
                                                                                                                                                                                                                                                                                                                                                              208 DCDPVF 213
                                                                                                                                                                                                                                                                          -CEEAF 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 AF 206
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Matches 5
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                                                                                                                         C; Species: Homo saplens (man)
C; Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C; Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C; Accession: 154182
R; Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen A; Reference number: 154182; MUID:93252381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumoriginic poxviruses: genomic organization and DNA sequence of the telomeric A;Reference number: A43692; MUID:87321103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDTVCATCAENSYNEHWNYLTICQLCRP-CDPVMGLEEIAPCTSKRKTQCRCQPGMFCAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LEIEFCLKHRSCPPGS-GVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 WALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQPHTRCENQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSVKQECNRTHNRVCECEEGRYLEIE-----FCLKHRSCPPGSGVVQAGTPERNTVCKK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LLVLLDIIEWTTQETLPP-----KYLHYDPETGHQLLCDKCAPGTYLKQHCTVR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 VLGLFGLLAASQPQAVPPYASENQTCRDQEKEYYEPQ--HRICCSRCPPGTYVSAKCSRI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHQ-----LLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKEL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
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C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                        receptor 2-related protein - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 244; DB 2;
Pred. No. 1.1e-09;
2; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM;600979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 GLVEAAPGTAQSDTTCKNPLE 215
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ilarity 26.9%;
Conservative 33
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Matches 59; Conservative
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-435 <RES>
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                                                                                             tumor necrosis factor
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                                                                                                                                                                                                                                                                                                                   66 TPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCK 125
                                                                                                                                                                                                                                                                                                                                                                                                                  284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYGDVICSPCGFGTYSHIVSSADKCEPVPN-NTFNXIDVEITLXPVNDTSCT----RTIT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 LGHSNLTTEQLLALMESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKG 344
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 YDPETG-----HQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 YIPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WLCCALLVLLDIIEWTTQETLPPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLC
                                                                                                                                                                                                                                                                                                                                                                                         FCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 KGNATHDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAE
                                                                                                                                                                                                                                                                                          63 VPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI ---- E
                                                                                                                                                                                                                         :| | :: | :| | : | :| | FLSCIIINGRDAAPYT----PPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Species: variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-J
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.;
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of var.
A;Reference number: Z20488; MUID:94088747
A;Accession: T28623
A;Attus: preliminary; translated from GB/EMBL/DDBJ
A;Attus: Dreliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVERIKRRHSS-----QEQTFQLLK-----LWKHQNRDQEMVKKIIQDIDLCESSVQ
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-348 <MAS>
A; Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g
A; Experimental source: strain Bangladesh 1975
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAA60933.1; PID:q
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                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%; Score 215.5; DB 2; 23.1%; Pred. No. 8.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Mismatches 156;
                                                                                              9.9%; Score 216; DB 2; I 23.2%; Pred. No. 7.7e-08; tive 51; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --YRVGNVLDDDSHMPGSCDIHKLITNS--KPTRFL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMYALKHL--KTSHFP-----KTVTHSLRKTMRFL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 TLYPVNDTSCT----RTTTTGLSE--
                                                                                              Query Match 9.9%
Best Local Similarity 23.2%
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
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Best Local S
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G5 pecies: variola minor virus
C; Species: variola minor virus
S; Shchelkunov, S.N.; Tormenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
Submitted to Genbank, March 1998
A; Reference number: A7215
A; Reference number: A7215
A; Accession: D72175
A; Residus: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-34 cSHC>
A; Experimental source: strain Garcia-1966
A; Experimental source: strain Garcia-1966
                                                                                            A.Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
A.Cross-references: EMBL:X67117; NID:9516429
A.Experimental source: strain India-1967, isolate Ind3
R.Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A.71tle: Genes of variola and vaccinia viruses necessary to overcome the host protective
A.71tle: Genes of variola and vaccinia viruses necessary to sercome the host protective
A.Reference number: S32385; MUID:93202281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 CNNKGSSFKQLTKAKND--DGMMSHSETVTLAGDCLSSVDIYILYSNTNAQDYETDTIS- 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 FCLKHRSCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQ- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVERIKRRHSS-----GEQTFQLLK-----LWKHQNRDQEMVKKIIQDIDLCESSVQRH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 LGHSNLTTEQLLALMESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TITMNHTDCNPVFREEYFSVLNKVATSGFFTGENRYQNISK----VCTLNFEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLCCALLVLLDIIEWTTQETLPPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 FLSCIIINGRDAAPYT----PPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEI-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGNATHDNVCSGNREATQKCGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAE
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                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology F;32-66/Domain: NGF receptor repeat homology <NGF> F;68-109/Domain: NGF receptor repeat homology <NG2> F;110-151/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 217; DB 2; L; Pred. No. 6.6e-08; 51; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain India-1967, ssp. major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --YRVGNVLDDDSHMPGSCNIHKPITNS--KPTRFL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMYALKHL--KTSHFP-----KTVTHSLRKTMRFL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLYPVNDTSCT----RTTTTGLSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%;
                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 31-168 <SHC>
A; Cross-references: EMBL:X69198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                 A; Molecule type: DNA A; Residues: 1-349 <KOL>
                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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Best Local S
Matches 92
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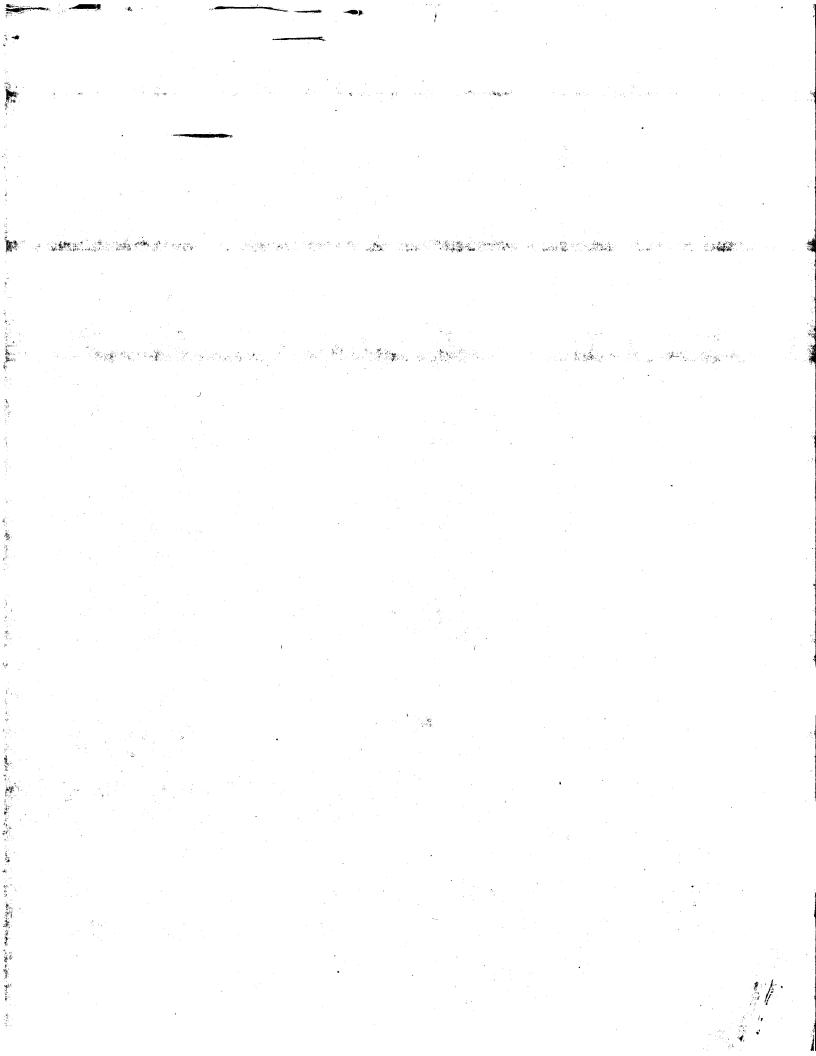
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 LLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LLVLLDIIEWTTQETLPPKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LILLIGVSLGGAKEACPTGLYTHSGE----CCKACNLGGGGVAQPCGA-NQTVCEPCLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 VTFSDVVSATEPCKPCTE-CVGLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEAC---R
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmenane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                   Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 SCPPGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 VCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nerve growth factor receptor precursor, low affinity
                                                                                                                                                                                                                                                                                                                               9.1%; Score 199; DB 1;
31.7%; Pred. No. 1.4e-06;
iive 25; Mismatches 71.
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22.1%; Pred. No. 1.8e-06;
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Best Local Similarity
Matches 52; Conserv
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Best Local 3
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Rxch. Biochem. Biophys. 294, 244-252, 1992
A; Title: Structural domains of the extracellular domain of human nerve growth factor rec A; Reference number: S21689; MUID:92198017
A; Reference number: S21689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.; Mercer, E.; Bothwell, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing of human melanoma nerve growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson, S.; Grob, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M21621; NID:9189206; PIDN:AAA36363.1; PID:9189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: nerve growth factor receptor; NGF receptor repeat homology C; Superfamily: nerve growth factor receptor; NGF receptor repeat homology C; Keyvords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; E; 12-28/Domain: signal sequence #status predicted <SIG> F; 29-427/Product: nerve growth factor receptor #status experimental <MAT> F; 29-55/Domain: extracellular #status predicted <EXT> F; 32-55/Domain: NGF receptor repeat homology <NG1> F; 57-108/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
C; Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
C; Accession: A2218; A60204; S21689; I57638
R; Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.;
Cell 47, 545-554, 1986
A; Title: Expression and structure of the human NGF receptor.
A; Reference number: A25218; MUID:87051725
    195 CGIDVTLCEEAFFRFAVPTKIIPNWLSVLVDSLPGTKVNAESVERIKRRHSS-----QEQ 249
                                                                                                                                                           250 TFQLLK-----LWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALMESLP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g189205
G.; Thompson
                                                                                                                                                                                                                      226 YFSVLNKVATSGFFTGENRYQNISK-----VCTLNFEIKCNNKGSSFKOLTKAKND--
                                                                                                                                                                                                                                                                                                                                                                                                      277 DGMMSHSETVTLAGDCLSSVDIYILYSNTNAQDYETDTIS---YRVGNVLDDDSHMPGSC
                                                                                                                                                                                                                                                                                                                           304 GKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHL--KTSHFP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A,Experimental source: melanoma cell line A875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-427 
A; Cross-references: GB:MI4764; NID:g189204; PIDN:AAB59544.1; R; Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, J. Neurochem. 48, 225-232, 1987
A; Fitle: Purification and amino terminal sequencing of human A; Reference number: A60204; MUID:87085574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nerve growth factor receptor precursor, low affinity - human
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A;Molecule type: DNA
                                                                                    ---SILTSEL
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A; Accession: 157638
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Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KTVTHSLRKTMRFL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 NIHKPITNS--KPTRFL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: NGF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 17q21-17q22
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A; Residues: 183-208 <VIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                    198 TGLSE-
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NA hternate names: NGF receptor
C; Alternate names: NGF receptor
C; Species: Gallus gallus (chicken)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
R; Large, T. H; Weskamp, G; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reicheuron 2, 1123-1134, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Status: preliminary: not compared with conceptual translation
A; Status: preliminary: not compared with conceptual translation
A; Molecule type: mRNA
C; Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c; Comment: This protein region of the extracellular domain may form part or all of C; Comment: This protein is thought to form a high-affinity receptor when it associates v C; Superfamily: nerve growth factor receptor; Molecule the type protein; receptor; treeptor; treeptor is predicted <SIG> Molecule tracellular #status predicted <SIG> Molecule tracellular #status predicted <SIG> Molecule traceptor repeat homology <MG1> MG2>
A; Molecule type: Molecule type traceptor repeat homology <MG2>
A; Molecule type: Molecule type traceptor repeat homology <MG2>
A; Molecule type: Molecule type traceptor repeat homology <MG2>
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A;Accession: JN0006
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A; Residues: 1-416 C-LARN
A; Experimental source: embryonic chick brain
R; Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A; Fitle: Structure and developmental expression of the chicken NGF receptor.
A; Reference number: A60504; MUID:90152140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: | : | | :: | 233 VITVMG-----SSQPVVTRGTIDNLIPVYCSILAAVVVGLVAYIAFKRWNSCKQNKQGA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSRPVNQTPPPEGEKLHSDSGISVDSQSLHDQQTHTQTASGQALKGDGNLYSSLPLTKRE 346
                                                                                                                                        -SYTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCECEEGRYLEIE--FCLKHRSCP 125
                                                                                                                                                                                                                           72 VIFSDVVSATEPCKPCTE-CLGLQSMSAPCVEADDAVCRCAYGYYQDEETGHCEACSVCE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---RECTPWADAE---CEEIPGRWIPRSTPPEGSDSTAPSTQEPEVPPEQDLVPSTVADM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QTFQLLKLWK--HQNRDQE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 MVKKIIQ-----LMESLPGKK-- 306
                                                                                                                                                                                                                                                                                                                             PGSGVVQAGTPERNTVCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNREATQKCGIDVTLCEEAFFRF-------A0NTK--IIPNWLSVL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ISPEEIER-TRKTCKSSEQLLKLLSLWRIKNGDQD--TLKG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 EVEKLLINGDTWRHLAGELGYQPEHIDSFTHEAC----PVRALLASW----GAQDSATLDA 398
18 LLLILGVSSGGAKETCSTGLYTHSGE-----CCKACNLGEGVAQPCGA-NQTVCEPCLDN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   F;240-261/Domain: transmembrane #status predicted <MEM>F;262-416/Domain: intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 VDSLPGTKVNAESVERIKRRHSSQE----
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SDAVCRCAYG-YFQDELSGSCKECSICEVGFGLMFPCRDSQDTVCEECPEGTFSDEANF 152
                                               Gaps
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                                                                                            41 CDKCAPGTYLKQHCTVRRKTLCVPCPDH-SYTDSWHTSDECVYCSPVCKELQSVKQECNR 99
                                                                                                                       Length 416;
                                               Indels
8.4%; Score 184; DB 1;
30.9%; Pred. No. 1.5e-05;
iive 28; Mismatches 67
                                                                                                                                                                                                                                                                                                              153 VDPCLPCTICEE-NEVMVKECTATSDAEC 180
                                                                                                                                                                                                                                                                             KAPCIKHTNCSTFGLLLIQKGNATHDNVC 185
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Best Local Similarity
Matches 46; Conserv
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OM protein - protein search, using sw model Run on: March 1, 2001, 09:20:05; Title: US-09-389-782A-5 Perfect score: 2240 Sequence: 1 ETFPPKYLHYDEETSHQLLC	r o o :	ompugen Ltd.  arch time 135.68 Seconds (without alignments) 345.542 Million cell updates/sec
	Gapop 10.0 , Gapext 0.5	

Total number of hits satisfying chosen parameters: 374700

374700 seqs, 117207915 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIE

					SUMMAKIES	
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Result		Query				
Ñ.	Score	Match	Match Length DB	DB	di.	Description
П	1013.5	45.2		4	000300	O00300 homo sapien
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m	893.5			11	008712	008712 mus musculu
7	877			11		008727 rattus norv
S	827			11	_	Q9rla4 mus musculu
9	433			4		095407 homo sapien
7	405.5			13		Q9pusO salvelinus
00	345			11		Q62327 mus musculu
σ	343.5			4		Q16042 homo sapien
10	338			11	088734	088734 mus musculu
11	297	13.3	655	4	075509	075509 homo sapien
12	280.5			13	Q90544	Q90544 ginglymosto
13	277.5			4	Q9UP60	Q9up60 homo sapien
14	273.5			4	09NPP6	Q9npp6 homo sapien
15	258.5			4	Q9Y6Q6	09y6q6 homo sapien
16	256.5			11	035305	O35305 mus musculu
17	241			12	057099	O57099 monkeypox v
18	239			12	057291	O57291 monkeypox v
19	239			12	057100	O57100 monkeypox v

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# ALIGNMENTS

RESULT	LT 1
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DE	OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
O E	(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
So	Homo sapiens (Human).
86	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Drimates: Catarrhin; Hominidae: Homo
o x	
N C	[1]
22	TISSUE-KIDNEY:
RX.	MEDLINE=97262071; PubMed=9108485;
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang MS.,
RA	oto
RA	
RA:	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA S	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
KA DEG	Suggly S., BOYLE W.U.; "Cetacorrotagarin. a novel secreted protein involved in the regulation
Į E	oreolytocegothin a mover secreted process since regularities of hone density ".
R.	Cell 309-319 (1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC E	TISSUE=LUNG FIBROBLAST;
2 Z	Maburana Solitoros), rummeu-9492009) Yasuda H., Shima N., Nakadawa N., Mochizuki ST., Yano K., Pufise N.,
RA	
RA	Tsuda E., Morinaga T., Higashio K.;
RŢ	"Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT	osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT	osteoclastogenesis in vitro.";
RI.	Endocrinology 139:1329-1337(1998).
R P	SEQUENCE FROM N.A.
22	TISSUE-PLACENTA;
КX	MEDLINE=98351569; PubMed=9688283;

us-09-389-782a-5.rspt

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Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
"Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
Eur. J. Biochem. 254.685-601(1998)
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
-!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
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                                                                                                                                                                                        -I-SUBCELLULAR LOCATION: EXTRACELLULAR.
-I-SUBCELLULAR LOCATION: EXTRACELLULAR.
-I-TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROLD, SPINAL CORD AND LIVER. ALSO DETECTED A NUMBER OF OTHER HEMATOPOLIFIC AND LIMMUNE ORGANS. NOT DETECTED THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
-I-SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. EMBL, AB00842; BAA32076.1; --
EMBL, AB00882; BAA32076.1; --
EMBL, U94332; AAB53709.1; --
EMBL, U94332; AAB53709.1; --
HSSP, P25942; LODE.
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EB42FA51C9D7C71E CRC64;
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PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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Matches 193; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE-PLACENTA;

TISSUE-PLACENTA;

TISSUE-PLACENTA;

"Cloning and Expression of Osteoprotegerin from Homo sapiens.";

Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).

EMBL; AF134187; AAF20168.1; -.

INTERPRO; IPR001368; -.

PROMOSTITE: PS00052; TNFR_OF:

PROSTITE: PS50050; TNFR_OF:

PROSTITE: PS50050; TNFR_NGFR_1; UNKNOWN_1.
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008712; 070202;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLRel. 15, Last annotation update)
03TEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
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Last annotation update)
                               241 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 281
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Higashio K.;
Higashio K.;
"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression nembryogenesis."

Gene 215:339-343(1998).

C. I. FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CO GSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMILATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
COSTEOCLAST OFFERENTY TROUPTING CELL-TO-CELL SIGNALING BETWEEN
COSTEOCLAST OFFERENTY PROPERIORS.
C. STRUMAL CELLS AND CSTEOCLAST PROGENITORS.
C. STRUMAL CELLS AND CSTEOCLAST PROGENITO
      PARAIN-BALBAC; TISSUE-KIDNEY;
MEDLINE-97262071; PubMed=9108485;
Missuer M.S., Lacey D.L., Dunstran C.R., Kelley M., Chang M.-S.,
Lucthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 TO DAY 17.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; 043131, AAB51308.1; -.
EMBL; AB013898; BAA32388.1; -.
EMBL; AB013899; BAA33388.1; -.
EMBL; AB013899; BAA33388.1; -.
EMBL; AB013900; BAA33388.1; -.
EMBL; AB013900; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R -> P (IN STRAINS 129/OLA AND NIH SWISS).
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
POTENTIAL.
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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SIMILARITY
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PROSITE: PS00652; TNPR_MGFR_1; UNKNOWN_1.

PROSITE: PS50017; DEATH_DOMAIN; 1.

PROSITE; PS50050; TNFR_NGFR_2; 2.

PRODOM; PD000771; -; 1.

Glycoprotein; Repeat; Cytokine; Signal.
SIGNAL
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                                                                                                                                                                                                        STRAIN=129/OLA, AND NIH SWISS;
MEDLINE=98382527; PubMed=9714833;
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INTERPRO; IPRO00488; -.
INTERPRO; IPRO01368; -..
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
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Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.
Davy E., Bucay N., Renshaw Geog L., Hughes T.M., Hill D., Pattison W.
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."

cell 89:309-319(1997).

cell B9:309-319(1997).

cell BS:309-319(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                    67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12. ETLPPRYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 LMESLPGKKISPEEIERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKHLKTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 -RIKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NKALPAPIEKTISKAKGOPREPOVYTL----PPSRDELTKNOVSLTCLVKGF
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
I -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                L -> R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --CGIDVTLCEEAFFRFAVPTK-----IIPNWLSVLVD---SLPGTKVN--AESVE-
                                                                                                                                                                                                                                                                                                                                          39.9%; Score 893.5; DB 11; Length 401; 47.8%; Pred. No. 1.1e-70;
                                                                                                                      S -> A (IN STRAINS 129/OLA AND
                                                         N -> D (IN STRAINS 129/OLA AND SWISS).
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.1e-70;
35; Mismatches 107; Indels
                                                                                                                                                                                                                                                CAA6102D3B312470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY----KCKVS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKTVT------HSLRKTMRFLHSFTMYRLYQKLFLE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLRel. 04, Created)
01-JUL-1997 (TrEMBLRel. 04, Last seq
01-OCT-2000 (TrEMBLRel. 15, Last anno
                            SMISS)
                                                                                                                                                      SMISS)
                                                                                                                                                                                                             SMISS
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MEDLINE=97262071; Pubmed=9108485;
                                                                                                                                                                                                                                                401 AA; 45923 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                      288
161
                                                         165
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NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --CGIDVTLCEEAFFRFAVPTK-----IIPNWLSVLVD---SLPGTKVN--AESVE--- 238
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              22 ETFPPKYLHYDPETGRQLLCDRCAPGTYLRQHCTVRRKTLCVPCPDYSYTDSWHTSDECV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCY-2000 (TrEMBLrel. 15, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                 -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U94330; AAB53707.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                               SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM)
                                                                                                                                                                                                                                                                                                                                                                                            Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Score 877; DB 11;
Pred. No. 3.2e-69;
3; Mismatches 52;
                                                                                                                                            SIGNAL 2 AVI OSTEOPROTEGERIN.
CHAIN 22 401 OSTEOPROTEGERIN.
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                                                                                                                                                                                                                                                                                  SIMILARITY.
SIMILARITY.
SIMILARITY.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.2%; Soc
Best Local Similarity 63.7%; Pro
Matches 165; Conservative 18;
                                                                                          INTERPRO; IPR001368; -. PFAM; PF00020; TNFR_C6; 4. PROSITE; PS00625; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; PRODOM; PD000771; -; 1.
                                                                                                                                                                                                                                                                                                                                                          46192 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AKTKPREEQYNSTYRVVSV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RIKRRHSSQEQTFQLLKL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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2201
365
54
62
80
80
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160
98
165
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107
144
306
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DISULFID
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DOMAIN
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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Betstein D., Ashkenazi A.; "Genomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                        170 STQKVDKTHT----CPP--CPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSH 222
                                                                                                                                                                                                                                                                                                                                                             223 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 282
                                                                                                                                                                                                                                                                                                                                                                                                                              283 PAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 ENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHECLHNHHTEKNLSHSPG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                            10;
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MEDLINE=99253915; PubMed=10318773;
Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LiCHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                           Length 437;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                          437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E).
                                                                                                                                                                                                                                                                       36.9%; Score 827; DB 11; I 60.9%; Pred. No. 8.8e-65; ive 44; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99087326; PubMed=9872321;
                                                                                                                                                                                                                                                                                                         Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 396:699-703(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Local Similarity
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EMBL; X76401; CAA53981.1; -.
HSSP; P19438; 1NCF.
     45.28;
                           71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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93
268
345
421
459 AA;
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Best Local Similarity
Matches 100; Conserv
     Best Local Similarity
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"A tumor necrosis factor receptor homolog is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation."; Biol. Reprod. 0:0-0(1999).

EMBL: AF156738; AAD56428.1; -.

INTERPRO; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                           Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DGR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DECOY RECEPTOR.
Salvelinus fontinalis (Brook trout).
Salvelinus fontinalis (Brook trout).
Actinopterygli; Neopterygli; Teleostei; Euteleostomi; Protacanthopterygli; Salmoniformes; Salmonidae; Salvelinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AA; 32679 MW; F90AEE33718449AF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
                                                                                                                                                            Sci. U.S.A. 97:1230-1235(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 433; DB 4;
Pred. No. 2.5e-30;
                                                                                                                                                                         EMBL, AF10419; AAD03056.1; EMBL, AF134240; AAD03056.1; EMBL, AF217796; AAF35244.1; EMBL, AF217796; AAF35244.1; EMBL, AF217796; AAF33686.1; EMBL, AF217794; AAF33686.1; EMBL, AF217794; AAF33686.1; EMBL, AF217794; AAF33686.1; EMBL, AF217796; AF33686.1; EMBL, AF217796; AF33686.1; EMBL, AF217796; AF33686.1; EMBL, AF00026; TWFR_C6; 4. FFAM; FF00020; TWFR_C6; 4. FROSITE; PS01186; EGF_2; UNKNOWN_1. PROSITE; PS01186; EGF_2; UNKNOWN_1. PRODOM; PD000771; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=20122600; PubMed=10655513;
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42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Conservative
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Best Local Similarity
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Proc. Natl.
EMBL; AF104
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SEQUENCE
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PROSITE;
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g à qq ò g Length 302;

DB 13;

Score 405.5;

18.1%;

Query Match

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12;
                                   5;
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                                                                                                                                                                                        71 YVKQECNRTHNRVCECKEGRYL--EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128
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                                                                                    DEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQ 70
                                                                                                                  27 DRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-MCAENO
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
                                      Indels
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T -> I.
S -> I.
S -> E.
Y -> C.
W; 6C5ID2CFIC4626DF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
Pred. No. 6.7e-28;
0: Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 345; DB 11; 25.2%; Pred. No. 2.3e-22; tive 53; Mismatches 164;
                                                                                                                                                                                                                                                                                                129 FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
                                                                                                                                                                                                                                                                                                                              :| :|:|| | :|| | :|| | 146 YSEVSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
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PPRAM; PF00020; TNER_G6; 4.
PROSITE; PS00055; TNFR_NGFR_1; 2.
PROSITE; PS00050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95178848; PubMed=7873884;
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VNCFILVQRKKKPSCLQRDA--KVPHVPDEKSQDAVGL---

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NCBI_TaxID=10090;
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01-NOV-1998 (
01-OCT-2000 (
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RESULT
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                                366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSES-TQKVDKTHTCP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 VICVVVDVSHEDP----EVKFNMYVDGVEVHNAK-TKPREEQYNSTYRVVSVLTVLHQD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK------N 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSLESSASALDRRAP----TRNQPQAPGVEASGAGEARASTGSSDSSPGGHGT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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   261 TVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
                     *EQUENCE FROM N.A.

*MEDLINE=91370690; PubMed=1966549;
Dembic Z.: Loctscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
Brockhaus M., Lesslauer W.;
"Two human TNF receptors have similar extracellular, but distinct
Cytokine 2:231-237(1990);
EMBL; $63368; AAB19824.1;
EMBL; $633681, AAB19824.1;
EMBL; $633681, AAB19824.1;
                                                                                                                                                                                                                         Euteleostomi;
Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBCBE329CC67FF6 CRC64;
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 343.5; DB 4;
Pred. No. 3e-22;
1; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 394
                                                                ::||:| | | : | | | : | 367 NVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 403
                                                 318 SLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 349
                                                                                                                                       439 AA
                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                         INTERPRO, IPR001368, -.
PFAM: PF00020; TNFR_c6, 4.
PROSITE: PS00552; TNFR_NGFR_1; 2.
PROSITE: PS00050; TNFR_NGFR_2; 3.
PRODOM: PD000771; -; 1.
SEQUENCE 439 AA; 46090 MW; FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                              TUMOR NECROSIS FACTOR RECEPTOR.
                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.8%;
Matches 107; Conservative 4
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                             sapiens (Human)
                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                  016042
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CSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGT 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;

"The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure and
Characterization of the two Transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHV-PDEKSQDAVGLEQQHLLTTAPSSSSS 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SL-------ESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRISDS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 -FLFPPKPKDTLMISRTPEVTCVVVD--VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 HYDEETSHQLLCDKCPPGTYLKQHCT-----AKWKTVCAPCPDHYYTDSWHTSDECLY 61
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRILIVSQPEPTRSQPIDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLIVGVTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GGPSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 RDELTKNQVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F6C15046B48FF83C CRC64;
                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , le-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 338; DB 11;
25.1%; Pred. No. 1e-21;
Live 50; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
  482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         655
                                          Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                          EMBL; Y14619; CAA74969.1; -.
EMBL; Y14620; CAA74969.1; JOINED.
EMBL; Y14621; CAA74969.1; JOINED.
EMBL; Y14622; CAA74969.1; JOINED.
EMBL; Y14623; CAA74969.1; JOINED.
EMBL; Y14679; CAA74969.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51106 MW;
                                        08,
08,
15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O75509 PRELIMINARY;
O75509;
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPRO01368; -. PFAM; PF00020; INFR_c6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.13
Best Local Similarity 25.1
Matches 102; Conservative
PRELIMINARY;
                                                        (TrEMBLrel. (TrEMBLrel.
                                                                                          P80 INF-ALPHA RECEPTOR
                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRODOM; PD000771; -;
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13;

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------KGNATHDNICSGN---SEST-----QKVDKTHTCPPCPAPELLGGP 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVSLLKP-PFEEIWTQQTATIVCEIV---YSDLENIKVFWQVNGVERKKGVETQNPEWSG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRD 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 DSWHTSDECLYCS-----PVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Galeomorphii, Galeoidea, Orectolobiformes,
Ginglymostomatidae, Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 EEWQSGVE-YTCSAKQDQSSTPVVKRTRKARVEPTKPHLRL---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|| || : :| || | : :| || || SKSTIVSKLKVWASEWDSGTEYVCLVEDSELPTPVKASIRKANVSQMHPPKVYLLHPSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 CPPGFGVVQAGTPERNTVCKRCPDGFFSNETS---SKAPCRKHTNCSVFGLLLTQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney, E.C., Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVEL ANTIGEN RECEPTOR.
2FF9D2071CDA6DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 280.5; DB 13; 26.5%; Pred. No. 1.7e-16; Live 53; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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Zheng S., Cao J., Cao W., Cai X., Geng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRWQQGNVFSCSVMHEALHN---HYTQKS 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 AEWNSDTTYSCLVGHPSLNRDLIRSTNKS 663
                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR003006; -. PFAM; PF00047; ig; 6. PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                         TISSUE=SPLEEN;
MEDLINE=95183140; PubMed=7877689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           684 N
75224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-OCT-2000 (TrEMBLrel.
SNC73 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
684 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                     Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 YRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 KELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : || | : || | 114 PWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS---GNSESTQKVDKTHTCPPC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED------PEVKFNWYVDG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI----EKTIS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC 66
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TNFR-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNFR-RELATED DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
Vincenz C., Aggarwal B.B., Dixit V.M.;
"Identification and functional characterization of DR6, a nove
domain-containing TMF receptor.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.3%; Score 297; DB 4; Length 65
28.3%; Pred. No. 5.9e-18;
Live 44; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF068868; AAC34583.1; -.
EMBL; AAL096801; CAB75692.1; -.
HSSP; PO7174; INCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NOVEL ANTIGEN RECEPTOR PRECURSOR.
Ginglymostoma cirratum (Nurse shark).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00020; TNFR_C6; 4.

PFAM; PF00531; death; 1.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655 AA; 71844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR000488; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50050; TNFR_
PRODOM; PD000771; -; 1.
                                                                                   DR6 OR DJ181J13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 KAKGQPR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 PIKGPKR 333
                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                 Parker A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Matches 8
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090544;
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Q90544
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  DDT REFERENCE OF THE PROPERTY 
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
                                                                                                                         ----KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                            | | | | : : | | | : : | | | PPPPCCHPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGP
                                                                                                                                                                                           246 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                              238 PERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLL
                                                                                                                                                                                                                                                         PPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AF018253; AAB86809.1; -.
HSSP; P25942; lCDF.
                                                         NCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHTCP-----PCPAPELLGGPSVFUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      142 TSSQLTLPATQ-----CPDGKSVTCHV-KHYTNPSQDVTVPCPVP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
RECEPTOR ACTIVATOR OF NF-K!
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           360 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPG 400
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TWFR-CYS 1.
TWFR-CYS 2.
TWFR-CYS 3.
TWFR-CYS 4.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P25942; ICDF.
MIM; 603499; -.
INTERPRO; IPR01368; -.
PFAM; PF00020; TNFR_G6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCED CYTOKINE RECEPTOR) (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
233
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                                                                                                                         PPKP----
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                            --TSSKAPCRKHTNCSVFGLLLTQK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 314
                                                                                                                                                                                                                                                                                       49 PDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQ- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TSSKAPCRKHT 143
                                                                                                                                                                                                                          Gaps
"Identification and characterization of SNC73, a gene which is down-regulated in colorectal cancer.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067420; AAC19365.1;
HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 LSLHRPALEDILLIGSBANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDK
                                                                                                                                                                                                                                                                                                                        GNATHDNICSGNSESTQKVDKTHTCP-----PCPAPELLGGPSVFLFPPKPK-----
                                                                                                                                                                                                                                                                                                                                                                                          -----DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
The European IMAGE consortium for integrated Molecular analysis
human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .69
                                                                                                                                                                                    Score 277.5; DB 4; Length 384; Pred. No. 1.6e-16; Mismatches 141; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.2%; Score 273.5; DB 4; Length 416; 27.9%; Pred. No. 4e-16; Live 37; Mismatches 140; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL389978; CAB97534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pluvinet R., Estivill.X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                 INTERPRO; IPRO03006; -. PFAM, PF00047; 19; 3. PROSTE; PS0047; 19, 3. SEQUENCE 300909; IC_MHC; UNKNOWN_1. SEQUENCE 384 AA; 40947 MW; BA7ADC3CA5A9DD48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBLrel. 15, Last sequence update)
MBLrel. 15, Last annotation update)
HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 PPGFGVVQAGTPERNTVCKRC-PDGFFSNE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 AA; 44786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                       12.4%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                    Query Match
Best Local Similarity 28.00
For 95, Conservative
                                                                                                                                                                                                                                                       PERNTVCKRCPDGFFSNE--
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Matches 95; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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RESULT 14

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4;
                                                                                                                                                                                                 77 NRTHNRVCECKEGRY--LEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETS 134
                                                                                                                                                                                                                                            20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC---KELQYVKQEC 76
BY SIMILARITY.
N'ILINED (GLCNAC. ..) (POTENTIAL).
N'ILINED (GLCNAC. ..) (POTENTIAL).
M'ILINED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                         Ouery Match
Best Local Similarity 34.5%; Pred. No. 1.3e-14;
Matches 58; Conservative 21; Mismatches 82; Indels 7
                                                                                                                                                                                                                                                                          135 SKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHTCPP 182
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86 BY
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124 BY
133 BY
151 BY
169 BY
194 BY
174 N -
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

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(without alignments)
315.295 Million cell updates/sec

US-09-389-782A-5 2240 1 ETPPPKYLHYDEETSHQLLC......VMHEALHNHYTQKSLSLSPG 400 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 seqs, 32294092 residues Searched:

88757 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	P01857 homo sapien		homo	homod	oryct	-	_	ratt	P03987 mus musculu	P01868 mus musculu	P20759 rattus norv	P01869 mus musculu	P01863 mus musculu	P01865 mus musculu	P20762 rattus norv	P01864 mus musculu	ratt	wns	P01867 mus musculu	P04220 homo sapien	mus m	P01871 homo sapien	P01872 mus musculu	P01854 homo sapien	P01855 rattus norv	P01873 mus musculu	P20333 homo sapien	P03988 oryctolagus	_	P01874 canis famil	•	7 mesocri	P20768 suncus muri
SUMMARIES	ID	GC1 HUMAN	GC2_HUMAN	GC4_HUMAN	GC3_HUMAN	GC_RABIT	GC2_CAVPO	GC3_MOUSE	GCB_RAT	GC3M_MOUSE	GC1_MOUSE	GC1_RAT	GCIM_MOUSE	GCAA_MOUSE	GCAM_MOUSE	GCC_RAT	GCAB_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	MUCB_HUMAN	EPC_MOUSE	MUC_HUMAN	MUC_MOUSE	EPC_HUMAN	EPC_RAT	MUCM_MOUSE	TNR2_HUMAN	MUC_RABIT	TNR2_MOUSE	MUC_CANFA		MUC_MESAU	MUC_SUNMU
	DB	: -																			Н			Н									7	1
	Query Match Length	330	326	327	290	323	329											322	336	405	391	421	424	455	428	429	476	461	458	474		479	454	457
	Query	ຸທ	н	0.7	9.0	41.2		7.8	9.7	7.6	9.9	9.9	9.9	6.3	6.3	5.9	5.8	5.3	4.7	4.7	16.3	6.1	6.1	5.8	5.8	5.8	2.6					•	4.9	4.8
dР	N S	5																														_	_	
		1234	1148.5	1136	1133.5	923	904.5	847.5	ω	841.5	820	820	820	812.5	812.5	804.5	801.5	791	777.5	777.5	365.5	361	360	354.5	353	353	349.5	345.5	340	340	338.5	335	33.	332.5
	CO .	1		m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29			32	33

P23085 heterodontu P23087 heterodontu	P01879 oryctolagus P23088 heterodontu	P23086 heterodontu	P01875 gallus gall	P23084 heterodontu	P01876 homo sapien	P20758 gorilla gor	P01877 homo sapien	P25942 homo sapien
HVC2_HETFR HVCS_HETFR	ALC_RABIT HVCM_HETFR	HVC3_HETFR	CD40_MOUSE MUC_CHICK	HVC1_HETFR	ALC1_HUMAN	ALC1_GORGO	ALC2_HUMAN	CD40_HUMAN
		<b>~</b> -		<b>н.</b> ,	٦,	-1	_	7
438 438	299 461	393	446	370	353	353	340	277
14.1	13.3 13.2	12.9	12.6	12.5	12.4	12.3	12.2	11.8
315.5	298 295	288	282.5	279.5	277.5	274.5	273.5	264
34 35	36	38	40	41	42	43	44	45

# ALIGNMENTS

UMAN STANDARD; PRT; 330 AA.  L-1986 (Rel. 01, Created) L-1986 (Rel. 01, Last sequence update) L-1999 (Rel. 01, Last sequence update) L-1999 (Rel. 38 Last annotation update) L-1999 (Rel. 38 Last annotation update) L-1999 (Rel. 38 Last annotation update) MMA-1 CHAIN C REGION.  sapiens (Human).  sapiens (Human).  sapiens (Human).  NDE-RZOM N.A.  NNE-BZ37428; PubMed-6287432;  nuclestide sequence of a human immunoglobulin C gammal gene inc Acids Res. 10:4071-4079(1982).  NNE-RZOM N.A.  NNE-RZOM N.A.  NNE-RZOM N.A.  NNE-RAM H.A.  NNE-	ده	~			· Ou			
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	IT 1 IUMAN GC1_HUMA	21-JUL-1 21-JUL-1 21-JUL-1 15-JUL-1 IG GAMMA	Lenel. Homo sap Eukaryot Mammalia	SEQUENCE MEDLINE= Ellison "The nuc	21 SEQUENCE MEDLINE= Cunningh Waxdal Maxdal Macal Sequential Macal Mac	SEQUENCE MEDLINE- Rutishau Edelman "The cov acid	Blochemi [4] SEQUENCE MEDLINE- PODSTING "The rul MODOCION Chymotry Peptides	LPJ SEQUENCE MEDLINE- SChmidt "Three-of structural Hoppe-Se [6] DISULFII MEDLINE-

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-82197621; PubMed=6804948;

Blison JW., Hood L.E.;

Ellison JG. Sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";

Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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                                                                                                                                                                                                                                                                                                                                                                                       Score 1234; DB 1; Length 330;
Pred. No. 6.1e-77;
4; Mismatches 6; Indels 10
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Best Local Similarity 92.1
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                                                                                                                                                                                       "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9 - and 2.54 resolution.";

Biochemistry 20:2361-2370(1981).

-!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS IN THE AMIDATION STATES OF 35.116,198,269 & 272.

-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 15.116,198,269 & 272.

-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 155,166,177,195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                     MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
I'Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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K -> R (IN GLM(3) MARKER).
/FIId-VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FIId-VAR_003887.
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REMOVED POST-TRANSLATIONALLY.
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MEDLINE-81208100; PubMed=7236608;
Deisenhofer J.;
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HINGE.
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Biochemistry 9:3188-3196(1970).
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MIM; 147100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95255298; PubMed-7737190; Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.; "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
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Milstein C., Franglone B.;
Tubsulphide bridges of the heavy chain of human immunoglobulin G2.";
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                                                                                                                              SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human 1962 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
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MEDLINE-80114419; PubMed=118920;
Hofmann T., Parr D.M.;
A note of the mino acid sequence of residues 381-391 of human
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              MEDLINE=81007873; PubMed=6774012; Wang A.-C., Tung E., Fudenberg H.H.; The primary structure of a human 1962 heavy chain: genetic, evolutionary, and functional implications."; J. Immunol. 125:1048-1054(1980).
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Mol. Immunol. 16:923-925(1979).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human immunoglobulin subclasses. Partial amino acid sequence of
Constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
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AT OR NEAR THE COMPLEMENT-BINDING
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    INTERCHAIN (WITH A HEAVY CHAIN)
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Pred. No. 3.7e-71;
3; Mismatches 8;
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PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
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(Rel. 38, Last annotation update)
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last anno
1G GAMMA-4 CHAIN C REGION.
                                                                                                                                                                 35884 MW;
                                                                                                                                                                                                                                       51.3%;
90.3%;
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326
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                                                                                                                  156
326
326 AA;
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Best Local Similarity
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P01861;
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1;
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                                                                                                                                                                                                                                                                 170 STQKVDKT-----HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 223
                                                                                                                                                                                                                                                                                 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 283
                                                                                                                                                                                                                                      Gaps
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Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                             NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Homo sapiens (Human).
Filarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 12-97 OF PROTEIN WIS.
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
HON (HEAVY CHAIN DISEASE PROTEIN) (HDC)
                                                                        INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                  INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                       Length 327;
                                                                                                                                                                                                                                    11; Indels
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                                                                                                                                                              MW; 3EDBD811EF208E7A CRC64;
                                                                                                                                                                                                       Score 1136; DB 1;
Pred. No. 2.6e-70;
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MEDLINE-82247835; PubMed-6808505;
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             CH1.
HINGE.
CH2.
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MEDLINE-81021548; Pubmed-6774747;
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21-JUL-1986 (Rel. 01, Last seq
30-MAY-2000 (Rel. 39, Last ann
IG GAMMA-3 CHAIN C REGION (HEAN
                                                                                                                                                                                                       50.7%;
89.5%;
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247
327 AA;
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P01860;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                          -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CH1 REGION.
-!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
GAMMA-3 HEAVY CHAINS.
-!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                         MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN. MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                      OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
MISCELLANEOUS. THE HINGE REGION CHAINS AND CONTAINS THREE
IDENTICAL IS-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                       Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBUNIT: DIMER LINKED BY 12 DISULETDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULEIDE BOND AT POSTITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN DIMER).
CHAIN DIMER).
CHAIN DIMER).
Heavy chain disease in man: cDNA sequence supports partial
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DIMER)
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MISSING (IN ZUC).
/FTIG=VAR_003895.
F -> Y (IN OMM).
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CH2.
CH3.
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MIM: 147120; -
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
PFAM: PF00047; 19; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain;
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290
127
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             gene deletion model.
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"Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                     Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                              153 TQKGNATHDNICSGNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 212
                                                                                                                                            213 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSTYRVVSVLIVLHQDWLNGKE 272
                                                                                                                                                                                        102 VTCVVVDVSHEDPEVQEKWYVDGVQHVARTKPREQQENSTFRVVSVLTVLHQNWLDGKE 161
                                                                                                                                                                                                                         YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 332
                                                                                                                                                                                                                                                                       VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 392
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                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
0ryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=70110015; PubMed=5461106; Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.; "Sequence studies of the Fd section of the heavy chain of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.,
"Heavy chain genes of rabbit 19G: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                           49;
                                    Length 290;
                                                           Indels
 E69CBC95705B2F46 CRC64;
                                   ; Score 1133.5; DB 1;
; Pred. No. 3.4e-70;
19; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                      323 AA.
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SEQUENCE OF 1-128.
MEDLINE=76135469; PubMed=1243651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=84030930; PubMed=6313520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F-I haplotype.";
Immunogenetics 18:387-397(1983).
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 32331 MW;
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                                   50.6%;
70.8%;
                                                          Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 132-161.
290 AA;
                                               Similarity
                                                                                                                                                                                                                                                                                                                    KSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                          282 KSLSLSPG 289
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P01870;
SEQUENCE
                                    Query Match
                                                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 ---HTC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 VAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVUDVSODDPEVQFTWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                          MARKER,
D11 AND H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 DSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPG 322
                                                                                                                    -!- MISCELLANEOÚS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I -> M (IN D11 MARKER).

I -> A (IN E15 MARKER).

I -> A (IN REF. 2).

V -> VPV (IN REF. 2).

V -> C (IN REF. 3 AND 4).

V -> D (IN REF. 5).

V -> W (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M (IN D11 MARKER).

A (IN E15 MARKER).

E (IN REF. 2).

E (IN REF. 3).

D (IN REF. 5).

E (IN REF. 5).

E (IN REF. 5).

C (IN REF. 5).

C (IN REF. 5).

C (IN REF. 5).

D (IN REF. 5).

C (IN REF. 5).

C (IN REF. 5).

C (IN REF. 5).

D (IN REF. 5).

C (IN REF. 5).
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61.5%; Pred. No. 6.7e-56;
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P01862;
21-JUL-1986 (Rel. 01, Created)
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PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR000495; -. INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHRB
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173
187
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--HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG

**VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG** 

353

SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPG

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296 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD
                                                                                                             283 ADGSYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG
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            178
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                                                                                                                                                                                                                                  Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
                                                                                                                                                                                                [3]
SEQUENCE OF 69-133 AND 312-329.
MEDLINE-71058486; PubMed=5538616;
Turner K.J., Cebra J.J.;
"Structure of heavy of hain from strain 13 guinea pig
immunoglobulin-6(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Blochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                         SEQUENCE OF 4-68.
MEDLINE-71058471; Nubmed=5538606; J.J.;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                             SEQUENCE OF 134-226.
MEDLINE=75036072; PubMed=4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN).
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NON_TER 1 1 1

DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
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36074 MW; 5D231B7164D1FBA9 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2 CHAIN C REGION.
                                                                                      Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFIDE BONDS.
MEDLINE=71058474; PubMed=4922544;
                                                                                                                                                                                                                                                                                                                                                     3iochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 13:4804-4811(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 INBRED GUINEA PIGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000495; -.
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79
105
107
110
202
178
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SEQUENCE OF 227-311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
178
248
329 AA;
                                                                  [1]
SEQUENCE OF 1-3,
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 FGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC$G 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 NSESTQKVD----KTHTCP--PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.8%; Score 847.5; DB 1;
54.0%; Pred. No. 8.9e-51;
ive 47; Mismatches 72;
                                                                                    01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
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                       329
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HINGE.
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CH3.
                                                             01-AUG-1991 (Rel. 19, Created)
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 54.0 ses 162; Conservative
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR000495; -. INTERPRO; IPR003006; -. PFAM; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223
327
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                                                                                                                                                       Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 :
                                                                                       01-AUG-1991
15-JUL-1999
                GC3_MOUSE
P22436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
SEQUENCE
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GC3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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31;

53; Indels

Mismatches

30;

Conservative

Local Similarity

Query Match

Matches 173;

40.48;

Score 904.5; DB 1; Length 329; Pred. No. 1.2e-54;

-- 177 Gaps

127 GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT-----

61 GLYSLTSMVTVPSSQKATCNV------

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                                340
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 280
                                       341 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                       01-FEB-1991 (Rel. 17, Last sequence update)
15-JU1-1999 (Rel. 38, Last annotation update)
1G GAMMA-2B CHAIN C REGION.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          286
              149 SEDDPDVHVSWFVDNKEVHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNK 208
                                                                                                                                                                                                                               "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 354
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 P-----PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                        CHAIN).
CHAIN).
CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                  Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT----
                                                                                                                                                                                                                                                                                                                                                                                                                 53; Indels
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56.3%; Pred, No. 1.8e-50;
tive 38; Mismatches 53;
                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Immunoglobulin C region
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INTERCHAIN (
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INTERCHAIN (
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                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                        36497 MW;
                                                                                                                                                                                                                                                                       PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Matches 161; Conservative
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                       INTERPRO; IPR000495; -.
                                                                                                                                                                                                                                        Gene 74:473-482(1988).
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106
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112
115
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106
109
112
115
147
253
333 AA;
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SEQUENCE FROM N.A.
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DISULFID
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                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-85027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 398
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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                                                                                                                      15-JUL-1999 (Rel. 38, Last annotation update)
(GAMMA-3 CHAIN C REGION, MEWBRANE-BOUND FORM.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.6%; Score 841.5; DB 1;
53.8%; Pred. No. 2.8e-50;
ive 47; Mismatches 72;
                          398 AA
                                                                                                 01-AUG-1991 (Rel. 19, Last sequence update)
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CYTOPLASMIC
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Iransmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segment.";
Nucleic Acids Res. 11:6775-6785(1983).
                          PRT;
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
                                                                         23-OCT-1986 (Rel. 02, Created)
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PROSITE; PS00290; IG_MHC; 1.
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                          STANDARD;
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Matches 161;
                       GC3M_MOUSE
P03987;
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GC3M_MOUSE
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IPR003006; -.

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INTERPRO;
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 281 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 340
              SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed-6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE-80012837; PubMed-113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                 341 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 399
                                                                                                                                                                                                IG GAMAMA-I CHAIN C REGION.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                         MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                               "The disulphide bridges of a mouse immunoglobulin G1 protein."; Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                      324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain.";
Nucleic Acids Res. 6:3305-3321(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE-78242288; PubMed-98524;
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V00793; CAA24172.1; --
EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24175.1; --
EMBL; V00795; CAA24175.1; --
EMBL; V00795; CAA24176.1; --
EMBL; V00795; CAA24176.1; --
INTERPRO; IPRO00495; --
                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                             gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                             21-JUL-1986 (
21-JUL-1986 (
30-MAY-2000 (
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P01868;
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GC1_MOUSE
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Function M.;
Brueggemann M.;
Brolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
PIR, PS0017, PS0017.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STQKVDKTHT ----CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GC1_RAT STANDARD; PRT; 326 AA.
P20759;
01-FEB-1991 (Rel. 17, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, East annotation update)
16 GAWMA-1 CHAIN C RECION.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 ENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323
                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                 region; Glycoprotein;
                                                                                                                                                                                   CHAIN).
                                                                                                                                                                                                   CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                Length 324;
                                                                                                                                                                                                                                                                               REMOVED POST-TRANSLATIONALLY.
                                                                                                                                                                                                                                                                                                                                                                                                              39; Indels
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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Pred. No. 6.3e-49;
5; Mismatches 39.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C
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HINGE.
CH2.
CH3.
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HINGE.
CH2.
CH3.
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60.5%;
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PROSITE; PS00290; IG_MHC;
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102
102
1104
1109
1198
1174
1174
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278
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112
219
326
                                                                                 97
                                               Alternative splicing.
                                                                                                                                                                                                                                                                                             276
278
324 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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113
220
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DISULFID
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MOD_RES
CONFLICT
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3;

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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
"Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEGMENT OF MU CHAINS.
 MEDLINE-82222190; PubMed-6283537;
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DISULFID
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                           339
                                                                                                                                            Gaps
                                                                                                                                                                                                                         STQKVDKT-----HTCPPCPAPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                        280 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                     [1]

BEDUENCE FROM N.A.

MEDLINE-80045036; PubMed-115593;

Honjo T... Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takabashi N., Mano Y.;
Takabashi N., Mano Y.;
Takabashi N., Mano Y.;
Takabashi N., Mano Y.;
Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
TYLER B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"mRNA for surface immunoglobulin gamma chains encodes a highly
"TYLER B.M., Transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Murinae; Mus
                                                                           N-LINKED (GLCNAC. ..) (POTENTIAL)
013BAB45EF49B9DA CRC64;
                                                                                                                                            14;
          HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
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                                                                                                                     36.6%; Score 820; DB 1; Length 326;
60.6%; Pred. No. 6.4e-49;
.ive 42; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 323-366 FROM N.A.
BEDLINE-82115295; PubMed=6799207;
ROGETS J., Chol E., Souza L., Carter C., Word C.J., Kuehl Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; E
Sciurognathi; Muridae;
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            4 4 4 A
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ID GCIM_MOUSE

AC P01869;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

E IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
         INTERCHAIN (WITH A INTERCHAIN (WITH A INTERCHAIN (WITH A INTERCHAIN (WITH A
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                    35946
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                                                                                                                      Query Match
Best Local Similarity 60.6
Matches 146; Conservative
82
102
106
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304
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions of its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for communities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STQKVDKTHT-----CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 222
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CHAIN)
CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.6%; Score 820; DB 1; Length 393; 60.5%; Pred. No. 7.9e-49;
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4CC88343B7A1CE27 CRC64;
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HINGE.
CH2.
CH3.
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                                                                                                                                                               EMBL, V00793; CAA24172.1; -. EMBL, V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -. PIR; B02159; GIMSM.
                                                                                                                                                                                                                                                                                                            PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 60.53
Matches 144; Conservative
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INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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358
393 AA;
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GCAA_MOUSE
ID GCAA_MOUSE
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-81198976; PubMed-6262729;
Yamawaki Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81223894; PubMed-6787604; Ollo R., Auffray C., Morchamps C., Rougeon F.; "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                        and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer."; Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                            Sikorav J.-L., Auffray C., Rougeon F.; "Structure of the constant and 3' untranslated regions of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse 1gG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain; Immunoglobulin C region.
           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-MAX-2000 (Rel. 39, Last annotation update)
IG GAMMA-2A CHAIN C REGION, A ALLELE.
                                                                                                                                                                                                           Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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DISULFIDE BONDS.
MEDLINE=73056887; PubMed=4565406;
                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=81076554; PubMed=6777755;
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PROSITE; PS00290; IG_MHC; 1.
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                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa;
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330 AA;
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                                                                                     133 TSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDK-----THTCPP-- 182
                                                                                                                  183 CPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 242
                                                                                                                                                                                                243 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 302
                                                                                                                                                                                                                                                                                   MEDILINE-8222190; PubMed=6283537;

Yamawaki-Katadoka Y., Nakai S., Miyata T., Honjo T.;

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

Proc. Natl. Robucts CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEGMENT OF MU CHAINS. THAT IS HOMOLOGGUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANBOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Fransmembrane; Alternative splicing.
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                                            Indels
    DB 1;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
36.3%; Score 812.5; DB 1
56.5%; Pred. No. 2.1e-48;
ive 34; Mismatches 58
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PROSITE; PS00290; IG_MHC; 1.
                                            Conservative
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MGD; MGI:96443; IGH-1.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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                    Best Local Similarity
Matches 157; Conserv
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P01865;
Query Match
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                                                                                                                                                                                                                                                                      133 TSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDK------THTCPP-- 182
                                                                                                                                                                                                                              71 ISSTWPSQSIT-CNV------AHPASSIKVDKKIEPRGPTIKPCPPCK 111
                                                                                                                                                                                                                                                                                                                                                            303 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 362
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                          243 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOV
                                                                                                                                                                                                                                                         183 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88166903; PubMed-3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                            POTENTIAL.

YOTOPIASMIC (POTENTIAL).
N-IINKED (GLCNAC. ..) (POTENTIAL).
AC38138BFAED3FFO CRC64;
                                                                                                                                                     36.3%; Score 812.5; DB 1; Length 399; 56.5%; Pred. No. 2.6e-48; Live 34; Mismatches 58; Indels 29;
               CHAIN).
CHAIN).
CHAIN).
              INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY
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m 1}
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GAMMA-2C CHAIN C REGION.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                               Ouery Match
Best Local Similarity 56.58
Matches 157; Conservative
                                                                                                                44020
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P20762;
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181 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 237
                                                                                                                                                                                                                                                                                                   238 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 297
                                                                                                                                                                                                            Gaps
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Э;
                                                                        INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                             Length 329;
                                              INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                            Indels
                                                                                                                                   5FCD7B7933850773 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 35.9%; Score 804.5; DB 1; Best Local Similarity 63.7%; Pred. No. 7.2e-48; Matches 142; Conservative 41; Mismatches 37;
HINGE.
                              CH3
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143
249
329 AA;
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1, 2001, 09:17:45 Search completed: March Job time: 263 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 1, 2001, 09:15:45 ; Search time 79.26 Seconds
 (without alignments)
 342.673 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-389-782A-5 2240 1 ETFPPKYLHYDEETSHQLLC.....VMHEALHNHYTQKSLSLSPG 400

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

35	Description	gamma -	heavy ch	gamma -	heavy	gamma chain C	g gamma-3 chain	Ig gamma-3 chain C	g gamma-2 chain	q qamma-4 chain	g gamma-3	6	ь	ь	6	Б	6		g heavy		g gamma-1	g gamma-	g gamma-2b		monoclonal antibod	Ig gamma-1 chain C	ь	6		Б
SUMMARIES	ΩI	СННО	S72664	S31866	869339	PT0207	A23511	A60764	G2HU	G4HU	G3HUWI	GHRB	147160	147159	147162	G2GP	147158	147161	S22080	C30554	S31459	G3MSC	PS0018	G3MSM	PC4436	GIMS	PS0017	G1MSM	G2MSA	G2MSAM
	DB	Н	7	4	7	7	7	7	-	-	<del>,  </del>	-	7	7	~	Н	7	7	7	~	7	Н	7	-	N	Н	7	-	Н	П
	Query Match Length	330	374	255	374	234	377	377	326	327	289	323	328	328	277	329	328	328	470	308	472	329	333	398	444	324	326	393	330	399
ø	Query Match	55.1	54.9	54.9	54.7	52.8	51,5	51,5	51.3	50.7	50.6	41.2	41.0	41.0	40.9	40.4	40.0	39.7	38.5	38.0	38.0	37.8	37.6	37.6	37.1	36.6	36.6	36.6	36.3	36.3
	Score	1234	1230	1229	1225	1183.5	1154.5	1152.5	1148.5	1136	1133.5		917.5	917.5	915.5	904.5	895.5	889.5	861.5	851.5	851.5	847.5		841.5	830	820	820	820	812.5	812.5
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Iq qamma-2a chain	Ig gamma-2c chain	Iq qamma 2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Iq qamma-2b chain	Iq qamma-2b chain	Iq qamma-2 chain C	Iq qamma-2b chain	Iq qamma heavy cha	Iq heavy chain V-I	Iq heavy chain VHI	Ig qamma-1 chain C	Iq Y heavy chain (	Ig heavy chain pre
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S37483	S00847 ·	S40295	G2MSAB	PS0019	G2MS11	GZMSBM	S25057	S06611	S01321	146732	A36040	S69340	S14236	B46529	S04845
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469	329	446	332	322	336	405	474	327	475	180	218	249	.152	572	549
36.3	35.9	35.8	35.8	35.3	34.7	34.7	34.7	34.2	33.7	31.3	25.6	25.6	25.3	17.7	16.7
812.5	804.5	802.5	801.5	791	777.5	777.5	777.5	166	755.5	702	574.5	572.5	266	397.5	374
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1
	Ig gamma-1 chain C region - human C;Species: Homo sapiens (man) C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jn-1999 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.: Berson, B.J.: Hood, L.E.
	Nucleic Acids Res. 10, 4071-4079, 1982 A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A; Reference number: A93433; MUID:82274238
	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-330 <ell> A; Cross-references: EMBL:217370 A; Cross-references: EMBL:217370 A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker A; Note: Lys-330 is removed after translation</ell>
	R;Harris, L.J. submitted to the EMBL Data Library, October 1992 A;Reference number: S33904 A;Accession: S36861
	A; Molecule type: DNA A; Residues: 2-330 <har> A; Cross-references: EMBL: 217370 R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.</har>
	Cell 29, 6/1-6/9, 1982 A.Title: Structure of human immunoglobulin gamma genes: implications for evolution of A;Reference number: S33887; WUID:83001943 A;Accession: S33887
	A; Molecule type: DNA A; Residues: 88-113;235-330 <tak> A; Cross references: EMBL:217370 B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma</tak>
	Dictionalisty 7. 3101-3100, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 1310, 13
•	A; Molecule type: protein A; Mesidues: 1-96, 'R', 98-135 <cun> A; Note: this sequence has the Glm(3) marker, 97-Arg R; Ruttshauser, U; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.</cun>
	DICCHEMISTIY 9, 3171-3101, 1970, ARILLE: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se A;Reference number: A90564; MUID:71064025 A;Contents: Eu
	A;Accession: A90564 A;Molecule type: protein A;Residues: 136-154, \Q',156-165, \Q',167-176, \Q',178-194,'N',196-197,'D',199-238,'E',2 A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R;Ponsting1, H.; Hilschmann, N.
	Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

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Gaps

275 248 335

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A) Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
Submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene produc
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
C;Species: Homo sapiens (man)
C;Dacte: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: $72664
S;Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A;Reference number: $72664
A;Accession: $72664
A;Accession: $72664
A;Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-374 <KHA>
A;Residues: 1-374 <KHA>
A;Residues: 1-374 <KHA>
A;Coss-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 GNATHDNICSGNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 GQGTLVTVCS----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKAKGQPREPQVYTLPPSKDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID:933068; PIDN:CAA49866.1; PID:933069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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A; Residues: 1-255 <FIL.
C; Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:C; Reywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor F;23-255/Region: human 19 gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
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Pred. No. 1.3e-68;
4; Mismatches 9;
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Pred. No. 1e-68;
2; Mismatches
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98.3%;
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Best Local Similarity 93.1%;
Matches 228; Conservative
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A.Residues: 1-96. YR., 98-197, D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A.Residues: 1-96. YR', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A.Note: this sequence has the Glm(3) and Glm(non-1) markers
B.Gall, W.E.' Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A.Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A.Reference number: A90565; MUID: 7064027
A.Contents: annotation; disulfide bonds
A.Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A.Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A.Title: Rule of antibody structure. The primary structure of monoclonal igG1 immunoglob
A.Reference number: A91667; MUID: 77070267
A.Contents: annotation; disulfide bonds
C.Genetics:
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                                                                                                                               A; Molecule type: protein
A; Residues: 1-34, 0', 36-96, K', 98-115, 0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Note: this sequence has the Glm(17) and Glm(1) markers
A; Note: this sequence has the Glm(17) and Glm(17) markers
B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl KOI
A; Reference number: A91723; MUID:83289131
A; Accession: A91723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268
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Pred. No. 6.6e-69;
4; Mismatches 6;
                                 A;Reference number: A91668; MUID:77070269
A;Contents: myeloma protein Nie
A;Accession: B91668
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Ig heavy chain V region precursor - human
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92.1%;
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Best Local Similarity 92.1
Matches 232; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: IGHG1
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R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986
A; Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region A; Reference number: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVIN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 CNRTHNRVCECKEGRYLEIEF------CLKHRSC---PPGFGVVQAGTPERNTYC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: X03604; GB: M12958; NID: 933070; PIDN: CAA27268.1;
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C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Juli C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
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                                                                                                                                                              PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 394
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Pred. No. 5.7e-64;
19; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNVNH-KPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSCDTPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
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20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Gene: GDB:IGHG3
A)Cross-references: GDB:119339; OMIM:147120
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A; Residues: 1-377 <HUC>
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Matches 228;
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                                                                                                                                                                                                                                  C;Accession: S69339
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease. A;Reference number: S69339; MUID:95262687
A;Accession: S69339
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C; Species: Pan troglodytes (chimpanzee)
C; Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C; Accession: PT0207
R; Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
MOL. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: PT0207; MUID:91287716
                                                                                                                                                       S69339

Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
  204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFNWYVDGVEVHNAKTKPREEQINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin F;48-117/Domain: immunoglobulin homology <IMM>
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                                     Length
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ilarity 94.4%; Pred. No. 5.7e-66;
Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score.1225; DB 2;
Pred. No. 2.7e-68;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.7%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 96.6
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-374 <KHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -234 <EHR>
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Matches 221;
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                                       351
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51.3%;
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Best Local Similarity 90.3
Matches 214; Conservative
       R; Hofmann, T.; Parr, D.M.
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    u) with an IGHG4 convert
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A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
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A; Residues: 1-326 < CELL>
A; Cooss-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Note: Lys-326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A; Reference number: A92809; MUID:81007873
A; Contents: myeLong protein Til
A; Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C; Accession: A93906; A92809; A90752; A93132; A02148
R; Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A; Reference number: A93906; MUID: 82197621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- DTPPPC 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 360
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                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                    Length 377;
    c2,
                                                                                                                                             Superfamily: immunoglobulin C region; immunoglobulin homology
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A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, GE:; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
                                                                                                                                                                                                                                                                                                                   Indels
    c3,
A; Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A; Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                 Score 1152.5; DB : Pred. No. 7.5e-64; 19; Mismatches 32
                                                                                                                    A; Residues: 1-377 <HUC>
C; Superfamily: immunoglobulin C region; immuno C; Seywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 CNRTHNRVCECKEGRYLEIEF----
                                                                                                                                                                                                                                                                    51.5%;
67.1%;
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Best Local Similarity 67.19
Matches 228; Conservative
                                                                                           A; Molecule type: DNA
A; Residues: 1-377 <HUC>
                                                                       A; Status: preliminary
                                               A; Accession: A60764
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My Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobuli A; Reference number: A93132; MuID:80114419
A; Roccession: A93132
A; Molecule type: protein
A; Residues: 238-275 < HOF>
B; Hofmann, T: Parr, D.M.
Submitted to the Atlas, March 1980
A; Residues: A94591
A; Recidence number: A94591
A; Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A; Note: the revised sequence differs from that shown in having 60-Ala and in the amid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amap position: 14932.33-14932.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into c;Superfamily: Immunoglobulin c region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM2>
F;33-202/Domain: immunoglobulin homology <IM3>
F;133-202/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;17-83,140-200.246-304/Disulfide bonds: interchain (to heavy chain) #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
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C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
C;Accession, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
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Biochem. J. 121, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A9053; MID:7203350
A; Contents: annotation; myeloma protein Sa, disulfide bonds
A; Reference number: A9053; MID:7203350
A; Contents: annotation; myeloma protein Sa, disulfide bonds
A; Frangione, B.; Milstein, C.; Dink, J.R.L.
Nature 221, 145-148, 196
A; Title: Structural studies of immunoglobulin G.
A; Title: Structural studies of immunoglobulin G.
A; Contents: annotation; Sa, disulfide bonds
A; Gene: GDB:119338; OMIM:147110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104
A;Accession: A90933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1148.5; DB 1;
Pred. No. 1.1e-63;
8; Mismatches 8;
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us-09-389-782a-5.rpr

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A; Molecule type: protein
A; Residues: 59-125, EB', 128-226, 228-289 < WOL>
A; Residues: 59-125, EB', 128-226, 228-289 < WOL>
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of the A; Notexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletiance number: A93915; MUID:82247835
A; Contents: heavy chain disease protein Omm
A; Accession: A93915.
                                                                                                                                                                                                                                                                                                                                               A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu A;Accession: A90198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-
A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
                                                                                                                                                                     A;Note: Cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form i R;Wolfenstein-Todel C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of A;Reference number: A90198; MUID:77021516
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other
idue segment (12-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 TQKGNATHDNICSGNSESTQKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VICVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 VEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 CLKHRSC---PPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAP-CRKHTNCSVFGLLL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: GDB:119339; OMIN:147120
A.Map position: 14492.33
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
C.Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
E.203-207.Obomain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolldone carboxylic acid (Gln) #status experimental
F:6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%; Score 1133.5; DB 1; Length 289; 70.8%; Pred. No. 8.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches 218; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: IGHG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                          C. Genetics:
A. Map position: 14932.33-14932.33
A. Introns: 99/1; 111/1; 221/1
C. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C. Superfamily: immunoglobulin c region; immunoglobulin homology
C. Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMI>F; 99-110/Region: hinge
F; 134-203/Domain: immunoglobulin homology <IMI>F; 240-307/Domain: immunoglobulin homology <IMI>F; 240-307/Domain: immunoglobulin homology <IMI>F; 240-307/Domain: immunoglobulin homology <IMI>F; 240-307/Domain: interchain (to light chain) #status experimental
F; 27-83,141-201,247-305/Disulfide bonds: #status predicted
F; 106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                           Partial amino acid sequence of the constant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 50.7%; Score 1136; DB 1; Length 327; al Similarity 89.5%; Pred. No. 6.6e-63; 212; Conservative 8; Mismatches 11; Indels
                                                    A. Residues: 1-327 <ELL>
A. Note: the sequence was determined from the germline gene R. Pink. J. R.L.: Buttery, S.H.; De Vries, G.M.; Milstein, C. Biochem. J. 117, 33-47, 1970
A. Title: Human immunoglobulin sublclasses. Partial amino ac A; Reference number: A90249; MUID:70207560
                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-30;81-326 <PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 212
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'Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 14/160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 355-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the CDNA sequence
A;Reference number: 14/158; MUID:95015845
A;Accession: 14/160
A;Accession: 14/160
A;Accession: I4/160
A;Accession: 14/160
A;Accession: I4/160
A;Accession: I4/160
A;Accession: I4/160
A;Gatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-328 <ARC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region: immunoglobulin homology
F;133-202/Domain: immunoglobulin homology
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Craces: Sus scrofa domestic pig)
Cracesion: 147159
Cracesion: 147159
Cracesion: 147159
Cracesion: 147159
Cracesion: 153, 3565-3573, 1994
Cracesion: 147159
Cracesion: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :| |||| |
---NHPATTTKVDKRVGT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ - - PENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.0%; Score 917.5; DB 2; Best Local Similarity 60.5%; Pred. No. 1.7e-49; Matches 176; Conservative 35; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.0%; Score 917.5; DB 2
60.5%; Pred. No. 1.7e-49;
tive 35; Mismatches 43
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Best Local S
Matches 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
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                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 129-131;155-172, 'D', 174-184,'A', 186,'E', 188-200,'D', 202-217,'E', 219-232,'Q',
A; Molec: this has the els allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E; 20-82, Domain: immunoglobulin homology <IM1>
          A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A;Reference number: A91749; MUID:84030930
                                                                                                                                                                                  el4 marker, 185-Thr
                                                                                                                                                                                                                                                                                         the Fd sections of rabbit immunoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 RCPDGFFS----NETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Complex: An immunoglobulin heterotetramer subunit consists of two hain disulfide bonds. In some cases, such as IgA and IgM, the subunit c;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulif F;20-82/Domain: immunoglobulin homology <IM1>F;130-199/Domain: immunoglobulin homology <IM2>F;130-199/Domain: immunoglobulin homology <IM2>F;136-303/Domain: immunoglobulin homology <IM2>F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                           A; Note: this sequence has the d12 allotypic marker, 104-Thr, and B; Pratt, D.M.; Mole, L.E. Bochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the FG section A; Reference number: A90290; MUID:76135469
A; Accession: A90290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.2%; Score 923; DB 1; Length 323; 61.5%; Pred. No. 7.5e-50; ive 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 61.5 Matches 177; Conservative
                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-323 <BER>
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PDGFFSNETSSKAPC----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDK---T 177

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                                                                                                                       pig immunoglobulin-G(2). III.
                                                                                                                                                                                                                                                              R; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II.
A; Reference number: A90359; MUID:71058486
A; Recession: A90359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uinea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Contents: annotation; disulfide bonds
A/Contents: annotation; disulfide bonds
A/Note: Cys-16 is involved in a heavy-light chain bond
A/Note: Cys-16 is involved in a heavy-light chain bonds
A/Note: Cys-16. Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred
C;Complex: An immunoglobulin heterotetramer subunit consists of two ident cal land ain disulfide bonds. In some cases, such as IgA and IgM, the subunits as ociat
C;Superfamily: immunoglobulin heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM2>
F;24-310/Domain: immunoglobulin homology <IM2>
F;24-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (ASD) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Ttile: Primary structure of the C-H3 homology region from guinea pig 1962
A;Reference number: A90385, MUID:75036073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Primary structure of the C-H2 homology region from guinea pig 1952
A;Reference number: A90384; MUID:75036072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKT
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                                    R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea
A;Reference number: A90352; MUID:71058471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 227-311 <TR2>
R; Ollveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 197.
A; Title: Interchain disulfide bridges of 9
A; Reference number: A90354; MUID:71058474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 69-133;312-329 <TUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R,Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 19
A;Title: Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 134-226 <TRA>
                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 4-68 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A90384
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Matches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gramma 4 chain constant region - pig (fragment)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Accession: I47162
N; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequences A; Reference number: I47158; MUID:95015845
A; Accession: I47162
A; Accession: I47163
A; Accession: I47163
A; Accession: I47164
A; Accession: I47164
A; Accession: I47165
A
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C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Reference number: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 HTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD 353
                                                                                                                                                                                                                                        KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTP 349
178 HTCPPCP-----APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 231
                                                                                                                    YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDGFFSNETSSKAPC----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDK---T 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 PSGLYSLSSMVTVPASSLSSKSYTCNV-------NHPATTTKVDKRVGT 49
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                                                                                                                                                                                                                                                                                                                                                       PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                        ;Gene: IgG4
;Superfamily: immunoglobulin C region; immunoglobulin homology
;82-151/Domain: immunoglobulin homology <IMM>
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ilarity 61.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: ]
C; Superfa
F; 82-151,
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pigs.

Db 283 ADGSYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329

Search completed: March 1, 2001, 09:15:46 Job time: 144 sec

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GenCore version 4.5
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```

OM protein - protein search, using sw model

March 1, 2001, 09:17:00 ; Search time 70.93 Seconds Run on:

(without alignments) 192.831 Million cell updates/sec

US-09-389-782A-5 2240 1 ETFPPKYLHYDEETSHQLLC......VMHEALHNHYTQKSLSLSPG 400 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

268485 seqs, 34193795 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp/AA1982.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp/AA1994.DAT * /SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:* A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseg/genesegp/AA1997.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA1998.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA1999.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA1999.DAT:*/SIDS1/gcgdata/geneseg/genesegp/AA2000.DAT:*

/SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT

### SUMMARIES

	Description	Fusion protein TNF	Sequence of a reco	Antigenic peptide	Human Fas antiqen	Plasmid pDC406/OX4	OX40/Fc mutein, C	Fusion protein of	Integrin beta-1 ch	Rabbit TGFbetaRII:	Amino acid sequenc	Human neurturin re	Human NTNR alpha a
	ID	R24016	R51003	W60037	W50287	R81882	W48976	Y68949	W70540	W73513	Y54063	W71603	Y80123
		13	15	19	18	16	19	21	19	19	21	19	21
	Query Match Length DB	485	518	376	376	438	438	764	963	388	388	664	664
,p	Query Match	66.7	66.4	60.4	59.7	59.5	59.5	57.2	56.1	55.9	55.9	. 55.8	55.8
	Score	1493	1488	1352	1337	1332	1332	1281	1256	1252.5	1252.5	1249.5	1249.5
	Result No.	н	7	m	4	2	9	7	80	6	10	11	12

Bovine LX-1 extra Rat neur urin rece Rat NTNR alpha and Human TGDbetaRI:F Amino acd sequenc Human ocytokine rec tICAM(453) IgG immu SVPH1-26 disintegr Human interleukin- Human interleukin- Human interleukin- Human interleuchin- Human interferon-b Id4 polypeptide. Antl-574 single ch IL4 Y124D/IgGl pro Human interferon-b IgGl polypeptide. Aggrecanase artifit Aggrecanase artifit Aggrecanase artifit IL-13/IL-4 dual tr CD2 binding LFA-3- Human transmembran Porcine CTLA-4-Ig Linkered human IgG Human Interleukin	1 cha: y huma d sequ
Y24153 W71604 W735124 Y54064 W335124 W735124 W71640 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W70797 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079 W7079	Y31669 Y31669 R43339 W49816
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$\begin{matrix} w & w & w & w & w & w & w & w & w & w $	
1248.5 1248.5 1248.5 1247.1 1245.5 1242.1 1243.5 1243.5 1243.5 1243.5 1238.5 1238.5 1237.5 1236.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 1237.1 12	1234 1234 1234
11111111111111111111111111111111111111	

## ALIGNMENTS

R24016 standard; Protein; 485 AA. 26-NOV-1992 R24016; RESULT R24016

(first entry) protein TNFRFc. Fusion

Tumour necrosis factor; TNF; IgG1; immunoglobulin G1. Location/Qualifier 1..252 Synthetic. Key Region 

/note= "human TNF extracellular receptor"

253..270 /note= "linker and hinge" 271..379 /note= "IgG1 CH2" 380..485 /note= "IgG1 CH3" Region Region Region

EP488170-A.

91EP-0120187. 26-NOV-1991; 03-JUN-1992

90DE-4037837. 28-NOV-1990;

(BEHW ) BEHRINGWERKE AG.

Lauffer L, Oquendo P, Zettlmeissl G;

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NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1992;
                                                                14-SEP-1993;
                      WO9406476-A.
                                           31-MAR-1994
                                                                                                                              Jacobs CA,
  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                         9
                                                                                                  The sequence is that of fusion protein TNFRFC comprising the extracellular domain of tumour necrosis factor (TNF) fused via a hinge region to the FC part of the heavy chain of human igGl. It may be used as part of a cell free receptor binding test which can be used for the identification of agonists, antagonists, antibodies, biological activity of soluble cellular receptors, functional analysis of modified ligands and diagnostic or therapeutic substances. See also R24017.
                                                                                                                                                                                                                                                                                                                                                                           69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                          103 dqvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvck 162
                                                                                                                                                                                                                                                                                                                                                                                                                            219 pvstrsghtgptpepstapstsfllpmgpsppaedpeepkscdkthtcppcpapellggp 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of a recombinant human (rhu) tumour necrosis factor receptor
                                                                                                                                                                                                                                                                            9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                              Cell free receptor binding test contg. recombinant fusion protein comprising carrier bound to fusion partner coupled to fixed support, and second, labelled binding partner, for receptor or antibody screening etc.
                                                                                                                                                                                                                                                                                                                                                             RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-------
                                                                                                                                                                                                                                                                                                                                                                                                         -----ESTQKVDKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                   Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor receptor; chimeric antibody molecule; immuglobulin.
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                  Score 1493; DB 13
Pred. No. 9.8e-87;
'; Mismatches 76
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                                                                                  Example; Fig 6; 24pp; German.
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65.0%;
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           WPI; 1992-185084/23.
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                     485 AA;
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Matches 291;
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                             Cell
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Cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein thating a mol. wt. of about 75-80 kDa. The clohing of the CDNA for Taving a mol. wt. of about 75-80 kDa. The clohing of the CDNA for TNFRI was described in Smith et al., Science 248:1019,1990. Clone I is contained in expression vector pcav/NOT-TNFR (ATCC.68088). A crecombinant chimneric antibody may be produced having TNFR sequences substituted for the variable domains of either or both of the immunoglobulin molecule heavy and light chains and having TNFR sequences cummodified constant region domains. A specific example of a TNFR/FC fusion protein is given in Q45225/R51003. The rhu TNFR:FC fusion gene was created by ligating the following fragments into a cloning vector: J an 867 bp Asp118-Pvu2 fragment from pCNV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR. 2) a 700 bp Styl-Spel fragment from plasmid pIXX498 coding for 232 AAs of the cottor contg. the FC fragment of human IgGl. Plasmid pIXX498 is a yeast expression vector contg. the FC fragment of human IgGl. Plasmid piXX498 is a peast expression the truncated TNFR with the human IgGl. 3) An oligo linker, to linker was created by PCR using primer Q45226, which encodes the 3' can of the truncated TNFR with the human IgGl. 3) An oligo linker, cond of the truncated TNFR with the human IgGl. 9) An oligo linker, cond of the truncated TNFR with freepfor and the 5' end of human IgGl. 257-237 of human IgGl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ESTQKVDKTHTCPPCPAPELLG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 yydq--taqmccskcspgqhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcsc 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dqvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvck 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating TNF mediated inflammatory diseases with TNF antagonist esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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63.3%; Pred. No. 2.2e-86;
ive 21; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 32-34; 47pp; English
93WO-US08666.
                                                                                   92US-0946236
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Best Local Similarity 63.3
Matches 285; Conservative
                                                                                                                                                                                                                                                          Smith CA;
                                                                                                                                                              (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                         WPI; 1994-118172/14.
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250

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334

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Gaps

26;

368 311 428

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CKELQYVKQE--CNRTHNRVCECKEGRYLEIEFCLKHRSCPP----GFGVVQAGTPERNT 119
                                                                                                                                                                                                                                                                                     120 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 299
                                                                                                                                                                                                                                             78 cdeghgleveinctrtgntkcrckpnffcnstvc---ehcdpctkcehgiikectltsnt 134
                                                                                                                                                                                                                                                                                                                                                                   180 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 239
                                                                                                                                               23 lhhdgqfchk----pcppgerkardctvngdepdcvpcqegkeytdkahfsskcrrcr-1 77
                                                                                                                        8 LHYDEETSHQLLCDKCPPGTYLKQHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV; apoptosis modulation; immunoglobulin G1 Fc; IgG1 Fc; fusion.
                                                                                                                                                                                                                                                                                                                                                                                        ----cdktht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
                                          Length 376;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 lyskltvdksrwqqqnvfscsvmhealhnhytqkslslspg 375
                                          DB 19;
                                        60.4%; Score 1352; DB 19
ilarity 67.3%; Pred. No. 5.5e-78;
Conservative 15; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fas antigen derivative/IgG1 Fc fusion.
                                                                                                                                                                                                                                                                                                                             135 kcke--egsrsnepks------
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/label= sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96JP-0135760.
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/label= r
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N-PSDB; V07004.
                                        Query Match
Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09742319-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W50287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart failure, ischemic restencies of the heart, liver or kidney, and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This represents the antigenic peptide has (nd29) containing the Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heart failure; kidney failure; graft-versus-host disease; antibody; myocardial infarction; ischemic restenosis; endotoxic shock.
                                                             ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "hFas antigen signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic peptide hFas (nd29) containing Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30..376
/note= "hFas (nd29) protein"
                                                                                                                                         371 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                488 wqqqqnvfscsvmhealhnhytqkslslspg 517
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Location/Qualifiers

Homo sapiens

1..16

Peptide Protein

Z

W60037 standard; Protein; 376

RESULT W60037

11-SEP-1998 (first entry)

Examples; Fig 5-9; 86pp; Japanese.

376 AA;

Sequence

system

MOCHIDA PHARM CO LID. OSAKA BIOSCIENCE INST.

(MOCH ) MOCHIDA (OSAB-) OSAKA BI

97JP-0262521. 96JP-0290459. 96JP-0351718.

31-OCT-1996; 27-DEC-1996;

97WO-JP03978

31-OCT-1997; 26-SEP-1997;

07-MAY-1998

WO9818487-A1

Yatomi T;

Suda T,

Nagata S,

WPI; 1998-271925/24

N-PSDB; V34430

93US-0097827

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23-JUL-1993;
                     23-JUL-1993;
                                                             Baum PR,
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                      Query Match
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W48976
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                                                                                                                                                                                                                                                                                                    CKELQYVKQE--CNRTHNRVCECKEGRYLEIEFCLKHRSCPP----GFGVVQAGTPERNT 119
                                                                                                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHYDEETSHQLLCDKCPPGTYLKQHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65
                                                                                                                                                                                                                                                                               lhhdgqfchk----pcppgerkardctvngdepdcvpcqegkeytdkahfsskcrrcr-1 77
         promotes apoptosis and is useful in treatment
                                                         The present sequence is a Fas antigen derivative/IgG1 Fc fusion, which contains a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted). The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, ey, diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                               VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKVDKTHT
                                                                                                                                                                                                                                                                                                                                                               kcke--egsrsnepks-----cdktht
                                                                                                                                                                                                                                                                                                                                                                                    CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                           NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                  Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
modified extracellular
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine; cell surface molecule; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTOKSLSLSPG 400
                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                             Pred. No. 4.8e-77; Mismatches 6
                                                                                                                                                                                                                  Score 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pDC406/OX40/Fc*; membrane glycoprotein.
                                       Disclosure; Fig 4; 102pp; Japanese.
antigen derivative containing
                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                  59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R81882 standard; Protein; 438
          low antigenicity, promot viral and other diseases
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                                                                                                                                                                                                                             Similarity 66.6
77; Conservative
                                                                                                                                                                                    376 AA;
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Matches 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 RIHNRYCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                                                                                                                                            vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 crecqpghgmvnrcdhtrdtlchpcetgfyneavnydtckqctqcnh--rsgselkqnct 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                                                                    This plasmid encodes an OX40/Fc antibody fragment mutein protein, and is used to express a soluble OX40/Fc mutein fusion protein for use in detecting cDNA clones encoding a OX40 ligand. The Fc fragment may be derived from human 19G1, and the plasmid may be used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell line. Culture supernatant was purified by affinity chromatography and this was used, together with labeled goat anti-human 19G to screen various cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ptqdtvcrcr-----pgtqprqdsgyklgvdcvpcppghfs--pgnnq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- QKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 elpstptlveprscdkthtcppcpapeaegapsvflfppkpkdtlmisrtpevtcvvvdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                                                                         also vec
in e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS--------EST#-
                                                                                                                                                                                                                                                New isolated DNA encoding the OX40 ligand polypeptide - als and host cells, used to produce recombinant ligand used in prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%; Score 1332; DB 16; 62.4%; Pred. No. 1.2e-76; ive 23; Mismatches 75;
                                                                                                               Goodwin RG;
                                                                                                                                                                                                                                                                                                                                                                  Example 2; Column 35-38; 26pp; English
                                                                                                               RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
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                                                                                                               Gayle
93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 62.49
Matches 262; Conservative
                                                                                                            Fanslow WC,
                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                              WPI; 1995-357992/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AA;
                                                                                                                                                                                                 N-PSDB; T00829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OX40/Fc mutein
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10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shutter JR,
                                                                                                                                                                                                                                                                                                Chimeric
Chimeric
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Protein.
                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strokes
                                                                                                                                                                                   Y68949;
                                                                                                             378
           221
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                                                                                                                                            RESULT
Y68949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------QKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 ptqdtvcrcr-----pgtqprqdsgyklgvdcvpcppghfs--pgnng 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 elpstptlveprscdkthtcppcpapeaegapsvflfppkpkdtlmisrtpevtcvvvdv 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 ackpwtnctlsgkqtrhpasdsldavcedrsllatllwetqrptfrpttvgsttvwprts 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| || : | || || || :| : | :| || || 39 crecqpghgmvnrcdhtrdtlchpcetgfyneavnydtckgctqcnh--rsgselkqnct 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                   Purified polypeptide OX-40 ligands - for co:stimulation of T-cell production and binding assays for OX-40 and homologues
                                                                                         human IgG1 antibody'
                                                                                                                                                                      "changed from Gly in wild-type to Ala in mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 438;
                                                                                                              to Ala
                                                                   "Extracellular domain of mouse OX40"
                                                                                                                                            t
C
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                                                                                                                                           in wild-type
                                                                                                             in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2e-76;
                                                                                                                                                                                                                                                                                                                   Goodwin RG;
                                                                                        /note= "Mutant Fc region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.5%; Score 1332; D 62.4%; Pred. No. 1.2e ive 23; Mismatches
                                                                                                             /note= "changed from Leu
                                                                                                                                          "changed from Leu
mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS
                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Col 37-40; 26pp; English.
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   Gayle RB,
                                                                                                                                                                                                                                                               93US-0097827.
95US-0494574.
                                                                                                                                                                                                                                             95US-0494574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.5%
Best Local Similarity 62.4%
Matches 262; Conservative
                                                                                207..438
                     sapiens.
                                                                                                                                           /note=
                                                                    /note=
                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                  Fanslow WC,
                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                 226
                                                                                                                                                              228
                                                                                                                                                                                                                                                                                                                                     WPI; 1998-427099/36.
                    - Homo sap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 AA;
                                                                                                                                                             Misc-difference
                                                                                                  Misc-difference
                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                              N-PSDB; V32636.
                                                                                                                                                                                                                                            22-JUN-1995;
                                                                                                                                                                                                                                                               23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                                                    US5783665-A
                                                                                                                                                                                                                        21-JUL-1998
                   Chimeric
Chimeric
chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                 Baum PR,
                                                 Key
Region
                                                                               Region
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in the control of endothelial cell biology. The murine polynocleotide was identified from a white adipose tissue cDNA library. The polypeptide is useful for identifying receptors, which bind to and/or are activated by the polypeptide. The polynocleotide is useful in gene therapy of cerebral autosomal dominant ateriopathy with subcortial infarcts and leucoencephalopathy, an autosomal dominant disorder causing ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell development cycle protein of delta family useful for treating various disorders associated with central nervous system e.g. cerebral autosomal dominant ateriopathy and ischemic strokes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a fusion protien of the extracellular domain of a murine polypeptide, which a member of the cell development cycle protein family known as the Delta family of mammalian membrane surface-bound ligands, and the human immunoghobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G (IgG) Fc portion. The murine delta-related protein gene is expressed within vascular endothelium indicates a role for the polypeptides
                                                                                                                                                                                 341 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell development cycle; Delta family; membrane surface-bound ligand; endothelial cell biology; gene therapy; subcortial infarct; cerebral autosomal dominant ateriopathy; leucoencephalopathy; lschemic stroke; chimera
                                     SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                           ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein of murine delta-related protein and human IgG F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "extracellular region of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              delta-related protein"
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/note= "human IgG Fc portion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Mus sp.
- Homo sapiens.
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YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPHV
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                                                                                                                                                                                                                            Sequence
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                                           15;
                                                                                                                                                                                                                                                                                                                                                                                     Integrin; beta-1 chain; immunoglobulin; chimeric; heterodimer complex;
inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
                                                                   446
                                                                                                                                                                                                             307
                                                                                                                                                                                                                                                 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD 367
                                           Gaps
                                                          --PCPDHYY 49
                                                                                       TDSWH-----TSDECLYCSPVCKELQYVKQECNRTHNRVCECKEG-----RYLEIEFCL 98
                                                                                               EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                    KHRSCPPGFGVVQAGT---PERNTVCKRCPDGF-----FSNETSSKAPCRKHINCSV
                                                                                                                                   r-spcahg----gtchdlengpvc-tcpagfsgrrcevrithdacasgpcfngatc--
                                                                                                                                                                ----ytglspnnfvcncpygfvgsrcefpvglppsfpaaaepkscdkthtcppcpape
                                                                                                                                                  FGLLLTQKGNATHDNICS-----GN-----SESTQKVDKTHTCPPCPAPE
                                                                                                                                                                               LLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                           94;
                            Length 764;
                                           Indels
                                          99
                            DB 21;
                           Score 1281; DB 21
Pred. No. 3.6e-73;
; Mismatches 66
                                                                                                                                                                                                                                                                       KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
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/note= "signal peptide"
21..963
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "mature protein"
                                                                                                                                                                                                                                                                              DEETSHQLLCDKCPPGTYLKQHCTAKWKTVCA-
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                     57.2%; Sco...
59.6%; Pred
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97JP-0015118
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                      Integrin beta-1 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TORA ) TORAY IND INC.
                                    Similarity
       AA;
      764
                            Query Match
Best Local Simi
Matches 270;
                                                                                                                                                                                                                                                                                                                                                        26-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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29-JAN-1997;
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       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                        W70540;
                                                                                                                                                                                                                                                                                                                                                                                                    human.
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This represents an integrin beta-1 chain. The invention provides integrin-immunoglobulin chimmeric protein heterodimer complexes that comprises an integrin alpha or beta chain associated with an integrin alpha compared in particular with a chimeric proteins form heterodimer complexes, in particular with a chimeric protein containing an integrin beta chain and an immunoglobulin chain and an immunoglobulin chain, the integrin beta chain and an immunoglobulin chain; the immunoglobulin chain. The integrin alpha chain is preferably alpha 4 two may be a light chain. The integrin alpha chain is preferably alpha 4 transformed with vectors containing the DNA coding for the above chimeric proteins can be used in the preparation of the chimeric proteins and their heterodimer complexes. The heterodimer complexes, which are useful for testing potential promoters and inhibitors of the binding of (integrins to their ligands, function as blood platelet substitutes and hemostatics and as diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 dsfkirplgfteevevilgyicececqsegipespkchegngtfecgacrcnegrvgrhc 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                      Integrin-immunoglobulin chimeric protein heterodimer complexes as platelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YLKQHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAKWKTVCAPCPDHY-----YTDSWHTSDECLYCSPVCKELQYVKQ------EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---RVCECKEGRYLEIEFC-LKHRSCPP-----GFGVVQAGTPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --vck-ctdpkfggqtcemcqtclgvcaehkecvqcrafnkgekkdtctqecsyfnitkv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       674 esrdklpqpvqpdpvshckekdvddcwfyftysvngnnevmvhvvenpecptgpedpeep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 OKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 drsnglicggngvckcrvcecnpnytgsacdcsldtstceasnggicngrgicecg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 QKGNATHDNI----------CSGNS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETFPPKYLHYDEETS--HQLLCD------KCPPGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 56.1%; Score 1256; DB 19; Best Local Similarity 51.4%; Pred. No. 1.7e-71; Matches 272; Conservative 31; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Pages 50-57; 87pp; Japanese.
                                                                                                                                                                                                                                                                                                                      presence of plasma components
Tanaka T;
                                                                          WPI; 1998-427881/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRTHN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  963 AA;
                                                                                                                   N-PSDB; V33773
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of TGF-beta, especially fibroproliferative diseases, e.g. renal, intra-ocular or pulmonary fibrosis; diabetic nephropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koteliansky V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09965948-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                          370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a fusion protein of the rabbit transforming growth factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The encoded protein is an example of a protein of the invention, which are isolated TGF-beta receptor tusion proteins that competitively inhibit binding of TGF-beta receptor. The fusion protein can be used in a method for lowering the levels of TGF-beta in an individual having a trihitis. It can also be used to treat medical conditions such as fibroproliferative disorders. The fibroproliferative disorder is a kidney, intraocular or pulmonary fibrosis, especially selected from vitreoretinopathy, of momentonephritis, proliferative vitreoretinopathy, or myelofibrosis. The fusion proteins can also be used to treat collagen vascular disorders, including systemic sclerosis, collagen vascular disorders, including systemic lupus erythematosus. They can also be administered following coronary angioplasty, to prevent restenosis or scarring and reclosing of arteries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                  Transforming growth factor-beta receptor; TGF-beta receptor; arthritis; fusion protein; fibroproliferative disorder; diabetic nephropathy; glomerulonephritis; prollferative vitracoretinopathy; myelofibrosis; collagen vascular disorder; therapy; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 RVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD-----GFFSNETSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 KAPCRKHTNCSVFG----LLLTQKGNATHDNICSGNSESTQK----VDKTHTCPPCPAPELL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 WKTVCAPCPDHYY----TDSWHTSDE-----CLYC---SPVCKELQYVKQECNRTHN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 wtriastipphygksvnndmmytdnngavkfpqlckfcdvrsstcdngkscmsncsit--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming growth factor-beta receptor fusion protein - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.9%; Score 1252.5; DB 19; Lengt. 65.7%; Pred. No. 1e-71; ive 17; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanicola-Nadel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koteliansky V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 18-19; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treat fibroproliferative disorders
              W73513 standard; Protein; 388 AA.
                                                                                                                Rabbit TGFbetaRII:Fc protein.
                                                                                                                                                                                                                                                                                                                                              98WO-US07587.
                                                                                                                                                                                                                                                                                                                                                                                97US-0044641.
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gotwals P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-609994/51
                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOJ ) BIOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 AA;
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                                                                              02-MAR-1999
                                                                                                                                                                                                                                                                                                                                              16-APR-1998;
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W73513
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NAMES OF COLOR OF STREET STREE

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Splice variant; rabbit; transforming growth factor-beta; TGF-beta; type II receptor; Fc portion; human 1gG1; fusion protein; arthritis; fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis; diabetic nephropathy; qlomerulonephritis; collagen vascular disease; proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis; polymyositis; scleroderma; dermatomyositis; systemic lupus erythematosus; restenosis; wound; connective tissue production; adhesion; scarring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a splice variant of a rabbit transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth factor-beta (TGF-beta) type II receptor fused to the FC portion of human IgG1. The fusion protein has higher affinity for TGF-beta than fusion proteins comprising the non-variant form of the receptor. The fusion protein contains soluble TGF-beta receptor constructs that are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TGF-beta. The protein competitively inhibits binding of TGF-beta to cellular receptors and/or forms an inactive complex with TGF-beta. The protein is used to reduce levels of TGF-beta, for Ireatment of arthritic conditions associated with overexpression
                                                                                                                                              Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                   DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein of a splice variant of transforming growth factor-beta receptor, for inhibiting the growth factor, e.g. in treatment of fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cate R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y54063 standard; Protein; 388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0089452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 post-radiation fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gotwals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Z45251, Z45252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-106083/09
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glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disease, e.g. systemic sclerosis, polymyositis, scleroderma, dermatomyositis or systemic lupus erythematosus; and fibrosis associated with restenosis. It is also used for treating wounds, to prevent overproduction of connective tissus and so prevent adhesions or scarring, and to prevent post-radiation fibrosis (by administration to patients about to undergo radiation therapy).
                                                                                                                                                                                                                                                                                                                                                                                       236
                                                                                                                                                                                                                                                                                                        136 KAPCRKHTNCSVFG---LLLTQKGNATHDNICSGNSESTQK---VDKTHTCPPCPAPELL 189
                                                                                                                                                                                                                                                                                                                      RVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD-----GFFSNETSS 135
                                                                                                                                                                                                                                                                              sice-----kahevcv---avwrkndenitletvchdpklayhgflledsas 118
                                                                                                                                                                                                                                                                                                                                                                                                                 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSR 309
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                   | :: | | : | | | : | | | | wtriastipphyksvnndmmvtdnngavkfpqlckfcdvrsstcdngkscmsncsit-- 74
                                                                                                                                                                                                   37 WKTVCAPCPDHYY----TDSWHTSDE-----CLYC---SPVCKELQYVKQECNRTHN 81
                                                                                                                                                                                                                                                                                                                                                                         Human neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurturin receptor alpha; NTNR-alpha; variant; chimeric; protein; immunoadhesion; ret-expressing cell; neurological;
                                                                                                                                                                                                                                                                                                                                                           GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                Length 388;
                                                                                                                                                                          Indels
                                                                                                                                                DB 21;
                                                                                                                                     Score 1252.5; DB 21;
Pred. No. 1e-71;
                                                                                                                                                                         17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
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                                                                                                                                                55.9%;
65.7%;
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97US-0802805.
97US-0871913.
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                                                                                                                                                                         Matches 257; Conservative
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                                                                                                                                                            Similarity
                                                                                                        388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                         Sequence
                                                                                                                                                Query Match
                                                                                                                                                              Local
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The property of the property of the property of the present invention. NTRR-alpha proteins can be used: (a) to identify present invention. NTRR-alpha proteins can be used: (a) to identify and concleutes that bind specifically to it (potential agonists and antagonists) and to purify such compounds; (b) to modulate response of cells to neurturin (NTN); (c) to increase survival of Ret-expressing cells or to activate Ret on the surface of cells (soluble glial derived neurotrophic factor receptor (GDRR alpha) may be used the same way); (d) to increase the half-life of cognate ligands (especially NTN); (e) diagnostically to determine serum levels of its ligands; and (f) as an inmal feed additive or molecular weight marker. NTNR-alpha, its genes, corrections related to abnormal NTN activity or response, particularly neurological (central or enteric), renal or hematopoietic (spleen) diseases or injuries. Ab may be agonists or antagonists for therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-alpha expression, e.g. in some tumours), also reagents for immunoassay and affinity purification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 ncrasyqtvts-cpadnyqaclgsyagmigfdmtpnyvdssptg---ivvspwc----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --scrgsgnmeeece--kflr-dftenpclrnaigafgngtdvnvspkgpsfgatgaprv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNSESTOKVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVKFINMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related nucleic acid - useful for increasing survival of ret-expressing cells for treating e.g. neurological, renal and haematological diseases
                                                                                                                                                                                                        The present sequence represents human neurturin receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1249.5; DB 19; Lengtl; Pred. No. 3e-71; 23; Mismatches 57; Indels
                                                                                                                                                                     English,
Rosenthal A;
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                                                                                                                                                                     3; Page 81-83; 116pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y80123 standard; Protein; 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.64
Matches 264; Conservative
 Klein RD,
                                 WPI; 1998-467175/40.
N-PSDB; V58006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 AA;
 Hynes MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                       Example
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609 kttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg 663
                                                                          Y24153 standard; Protein; 445
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                                                                                                                                                                                                                                                        Chimeric - Bos sp.
Chimeric - Homo sapiens.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 AA;
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                                                                                                                                     10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kakutani M,
                                                                                                                                                                                                                                                                                                                                   01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1997
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Y24153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a neurturin receptor alpha (NTNR alpha). NTNR alpha binds neurturin. The NTNR alpha nucleic acid molecule is useful for the expression of NTNR alpha, which may be used to identify agonist and antagonist compounds having therapeutic applications, such as enhancing splenic haematopolesis, treating anaemia, thrombocytopaenia, hypoplasia, or haemorrhage. The present sequence is a NTNR alpha and IgG (immunoglobulin G) fusion protein from the
                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino acid sequence excluding the N-terminal signal peptide - .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 KQECNRTHNRVCECKEGRYLEIEF----CLKH------RSCP--PGFGVVQAGTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHD------NICS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ekt---pslpddlsdstslgtsvittctsvqeggl----kannskelsmcftelttniip 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YTDSWHTSDECLYCSPVCKELQYV 72
                                                         Human; neurturin receptor alpha; NTNR alpha; splenic haematopoiesis; anaemia; thrombocytopaenia; hypoplasia; haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | ||: ::| :| || ||:
--scrgsgnmeeece--kflr-dftenpclrnaiqafgngtdvnvspkgpsfqatqaprv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GNSESTQXVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 gprd---pvdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3e-71;
23; Mismatches 57; Indels
                               Human NTNR alpha and IgG fusion protein SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%; Score 1249.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Column 91-96; 78pp; English.
                                                                                                                                                                                                                                                                                                                  Klein RD;
                                                                                                                                                                                                           97US-0957063.
                                                                                                                                                                                                                                       97US-0038839.
97US-0049818.
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 (first entry)
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                                                                                                                                                                                                                                                                                                                Rosenthal A,
                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                              WPI; 2000-181808/16.
N-PSDB; 291459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 AA;
19-MAY-2000
                                                                                                      Homo sapiens
                                                                                                                                                                                                          24-OCT-1997;
                                                                                                                                                                                                                                      18-FEB-1997;
09-JUN-1997;
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hes 264;
                                                                                                                                                US6025157-A.
                                                                                                                                                                              15-FEB-2000
                                                                                                                                                                                                                                                                                                                  MA,
                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Matches
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                                                                  Bovine LOX-1 extracellular region/human IgG1 Fc region chimeric protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion peptide for assay of oxidized LDL and for therapeutic use
                                                                                                                                 LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia; low density lipoprotein; receptor; detection; immunoglobulin; fusion protein; chimeric protein.
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2e-71;
67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 75-79; 105pp; Japanese.
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(first entry)
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15-FEB-2000
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Synthetic.
                                                        Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTUR alpha)/Fc sequence (IFE2a) fusion protein, from an example of the present invention. NTUR-alpha proteins can be used: (a) to identify molecules that bind specifically to it (potential agonists and analogonists) and to purify such compounds: (b) to modulate response of cells to neurturin (NTN); (c) to increase survival of Ret-expressing cells or to activate Ret on the surface of cells (soluble glial derived neurotrophic factor receptor (GDNFR alpha) may be used the same way); (d) to increase the half-life of cognate ligands (especially NTN); (e) diagnostically to determine serum levels of its ligands; and (f) as animal feed additive or molecular weight marker. NTNR-alpha, its genes, (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo for treating conditions related to abnormal NTN activity or response, particularly neurological (central or enteric), renal or haematopoietic
                                           TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 320
 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 260
                     304
                                                       CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 380
                                                                                                   Human; neurturin receptor alpha; NTNR-alpha; variant; chimeric;
fusion protein; immunoadhesion; ret-expressing cell; neurological;
renal; haematological disease.
         Rat neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide(s) based on human neurturin receptor alpha and related nucleic acid - useful for increasing survival of ret-expressing cells for treating e.g. neurological, renal and haematological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents rat neurturin receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 84-86; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenthal A;
                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                       W71604
ID W71604 standard; Protein; 664
                                                                                                                                     400
                                                                                                                                                 425 vmhealhnhytqkslslspg 444
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97US-0802805.
97US-0871913.
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                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                    VMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-467175/40.
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                  WO9836072-A1
                                                                                                                                                                                                                                                               19-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                         W71604;
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201
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(spleen) diseases or injuries. Ab may be agonists or antagonists for therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-alpha expression, e.g. in some tumours), also reagents for immunoassay and affinity purification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 PERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHD-----NIC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vekt---pslpddlsdstslgtsvittctsiqeqgl----kannskelsmcftelttnis 430
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                                                                                                                                                                                                                                                                                                                                                                                       --GRYLEIEFCLKHRSCPPGFGVVQAGT 114
                                                                                                                                                                                                                                                                                          HCTAKWKTVCAPCP-DHY-------YIDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurturin receptor alpha; NTNR alpha; splenic haematopoiesis;
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ncrasyrtits-cpadnyqaclgsyagmigfdmtpnyvdsnptg---ivvspwc-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      --ncrgsgnmeeecekflrdftenpclrnaigafgngtdvnmspkgpslp----atgapr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 pg---srdpvdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 400
                                                                                                                                                                                              Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaemia; thrombocytopaenia; hypoplasia; haemorrhage.
                                                                                                                                                                                              DB 19;
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                                                                                                                                                                                                                                             61;
                                                                                                                                                                                      55.7%; Score 1248.5; DB 62.7%; Pred. No. 3.4e-71 ive 21; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein RD;
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                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                       73 KQECNRTHNRVCECKE----
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N-PSDB; 291460.
                                                                                                                                                                                                                    Similarity
                                                                                                                   664 AA;
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09-JUN-1997;
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                                                                                                                                                                                                               Local Simites 261;
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PT Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino XX Sclaim 3; Column 97-102; 78pp; English.

CC The present invention describes a neurturin receptor alpha (NTNR alpha).

CC WINR alpha binds neurturin. The NTNR alpha, which may be used to identify agonist and antagonist compounds having therapeutic applications, such as enhancing splenic haematopolesis, treating anaemia, cc thrombocytopaenia, hypoplasia, or haemorrhage. The present sequence is a NTNR alpha and IgG (immunoglobulin G) fusion protein from the present invention.

XX Sequence 664 AA;
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11; 378 vekt---pslpddlsdstslgtsvittctsigeggl----kannskelsmcftelttnis 430 73 KQECNRTHNRVCECKE---------GRYLEIEFCLKHRSCPPGFGVVQAGT 114 --ncrgsgnmeeecekflrdftenpclrnaigafgngtdvnmspkgpslp----atgapr 377 115 PERNITVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHD------NIC 164 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 284 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 344 Gaps 32 HCTAKWKTVCAPCP-DHY------YTDSWHTSDECLYCSPVCKELQYV 72 Length 664; 73; 61; Indels DB 21; 55.7%; Score 1248.5; DB : 62.7%; Pred. No. 3.4e-71; 21; Mismatches Query Match 55.7% Best Local Similarity 62.7% Matches 261; Conservative 324 225 488 285 QQ 셤 ð a οy g ŏ δ g δ g δ

Search completed: March 1, 2001, 09:17:03 Job time: 221 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-389-782A-6 2274 1 ETFPPKYLHYDEFTSHQLLC.....VMHEALHNHYTQKSLSLSPG 406 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 374700 seqs, 117207915 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

sp_archea:*
sp_bacteria:*
sp_human:*
sp_human:*
sp_nammal:*
sp_mammal:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* SPTREMBL_15:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

		Description	Oqubba homo sanien	00300 homo sapien	008712 mus musculu	008727 rattus norv	O9rla4 mus musculu	095407 homo sapien	s0 salvelinus	016042 homo sapien .	27 mus musculu	088734 mus musculu	075509 homo sapien	0 homo sapien	Q90544 ginglymosto	6 homo sapien	05 mus musculu	6 homo sapien	O57099 monkeypox v	91 monkeypox v	
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121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTV 180

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STRAIN-BALB/C; TISSUE-KIDNEY;
MEDLINE-97262071; PubMed-9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Lucthy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
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EB42FA51C9D7C71E CRC64;
Cytokine; Signal.

BY SIMILARITY.

OSTEOPROTEGERIN.
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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POTENTIAL.
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MEDLINE=98382527; PubMed=9714833;
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  31ycoprotein;
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181 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 201

YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV

22 61 284

292 TEQLLALMESLPGKKISPEETERTRKTCKSSEQLLKLLSLWRIKNGDQDTLKGLMYALKH 351

| : | | | : | | | : 352 LKTSHFPKTVT-----HSLRKTMRFLHSFTMYRLYQKLFLE 387 328 LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 373

285 -----PPSRDELTKNQVSLTC

236 SVE----RIKRRHSSQEQTFQLLKLWKHQNRDQEMVKKIIQDIDLCESSVQRHLGHSNLT

241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY-----KCKVS-----

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                  Tructure of the mouse osteoclastogenesis inhibitory factor (OCIF)

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GENERALIASIS 334341498).

CI- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES

OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY

SYMMHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO

OSTEOCLASTOGENESIS BY INTERPTING CELL-TO-CELL SIGNALING BETWEEN

CI- SUBMOLIT: HOMODIMER (MAJOR PORM) AND MONOMER (MINOR FORM).

CI- SUBMOLIT: HOMODIMER (MAJOR PORM) AND MONOMER (MINOR FORM).

CI- SUBMOLIT: HOMODIMER (MAJOR PORM) AND MONOMER (MINOR FORM).

CI- SUBMOLIT: STREESEED AT HIGH LEVELS IN LIVER, LUNG,

BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND

PLACENTA. NOT DETECTED IN SPLEEN.

CI- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT

CI- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT

CI- DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; 094331; AAB53708.1; -.
EMBL; AB013899; BAA28269.1; -.
EMBL; AB013909; BAA33388.1; -.
EMBL; AB013909; BAA33388.1; -.
EMBL; AB013900; BAA33388.1; -.
EMBL; AB013900; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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PROSITE: PS00652; TNRR_NGFR_1; UNKNOWN_1.
PROSITE: PS50017; DEATH_DOMAIN; 1.
PROSITE: PS50050; TNFR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
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INTERPRO; IPR000488; -
INTERPRO; IPR001368; -
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Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U94330; AAB53707.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOWODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
03-CCT-2000 (TrEMBLREN) (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
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 401
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PRAM; PR00020; TRRE_G6; 4.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
 PRT;
                                                                                                                                                                                                                                                               TISSUE=INTESTINE;
MEDLINE=97262071; PubMed=9108485;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      of bone density.";
Cell 89:309-319(1997).
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48.3%; Pred. No. 6e-73;
tive 35; Mismatches 102; Indels
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Matches 196; Conservative

Local Similarity

Query Match

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217 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bai C., Connolly B., Merzker M.L., Hilliard C.A., Liu X., Sandig V. Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99087326; PubMed=9872321;
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Owd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
"Genomic amplification of a decoy receptor for Fas ligand in lung
                                                                             REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99253915; PubMed-10318773;
Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LiGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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                                                                                                                                                                                                                                                                                               394 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHTTEKNLSHSPG 436
                                                                                                                                                                                                                                                                      364 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
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Last annotation update)
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PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS50050; TWFR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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MEDLINE=20122600; Pubmed=10655513;
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Proc. Natl. Acad. Sci. U.S.A. 97
EMBL; AF104419; AAD29681; -
EMBL; AF217796; AAF352441; -
EMBL; AF217793; AAF335851; -
EMBL; AF217794; AAF336861; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P25942; 1CDF.
INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
PFAM; PF00020; TNFR_C6; 4.
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AFI23372; AAD40243.1;
HSSP: P01842; TEAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 CPP--CPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 909; DB 11; Length 401; 85.6%; Pred. No. 9.1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEC6A31F1D4E573A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
  OSTEOPROTEGERIN.
                                              TWER-CYS 1.
TWER-CYS 2.
TWER-CYS 3.
TWER-CYS 3.
TWER-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9R1A4 PRELIMINARY, PRT, 43
O9R1A4;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequen
O1-OCT-2000 (TrEMBLrel. 15, Last annota
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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289
401 AA;
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Matches 154;
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Matches 140;
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"A tumor necrossis factor receptor homolog is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
Biol. Reprod. 0:0-0(1999).
Biol. Reprod. 8. AAD56428.1;
BSSP: P19438: LEXT.
                                                                    VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 124
                                                                              PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSG------NSESTQK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 YVKQECNRTHNRVCECKEGRYL - - EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128
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                                    64
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                                                                                                                   PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP
                                              11 DEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQ
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus. NCBI_TaxID=8038;
                   11;
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 DB 4; Length 300;
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                   Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
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Pred. No. 8.9e-28;
         .1e-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
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                                                                                                                                                                                                        302 AA.
                 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Mismatches
19.1%; Score 433.5; 39.1%; Pred. No. 3.1
                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00020; TWFR_C6; 4.
PROSITE; PS00652; TWFR_WGFR_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS50050; TWFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439
                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                            Salvelinus fontinalis (Brook trout).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71; Conservative
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                        PRELIMINARY;
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         Similarity
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                                                                                                                                         174 CGID 177
                                                                                                                                                           214 AVID 217
   Local S...
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SEQUENCE
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Query Match
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Q9PUSO;
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Q16042;
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---EVICVVVDVSHEDP----EVKFNWYVDGVEVHNAK-TKPREEQYNSTYRVVSVLTV 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK----- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKC-----GI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVTVDKTHTCP---PCPAPE----LLGGPSVFLFPPKPKDT-----LMISRTP---- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 PVSTRSQHTQPTPEPSTAPSTSFLLPMGPS----PPAEGSTGDFALPVGLIVGVTALGLL 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gap
                                                                                                                                                                                                                                                                                       MEDLINE-91370690; PubMed-1966549;
Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
Brockhaus M., Lesslauer W.;
                                                                                                                                                                                                                                                                                                                                             "Two human TNF receptors have similar extracellular, but distinct lintracellular, domain sequences.";
Cytokine 2:231-237(1990).
EMBL; 563368; AAB19824.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Mismatches 162;
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Pred. No. 3.8e-22;
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PFAM; PF00020; TNFR_c6; 4.
PROSITE; PS00062; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PRODOM; PD000771; -; 1.
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27.3%;
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                                                                                                                           Homo sapiens (Human).
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Best Local Similarity
Matches 110; Conserv
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Homo sapiens (Human).
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Mammalia; Eutheria;
                                                                                                                       482 AA;
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                                                                                                                                                                                                                                                                                              LQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGTPERNTVC 121
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                                                                                                                                                                                                                                                      9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                 Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
"The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure and
Characterization of the two Transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                263 GLVNCFILVQRKKKPSCLQRDA--KVPHVPDEKSQDAVGL------EQQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 VLTVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                   78;
                              receptor
                                                                                                                                                                                                               Length 459;
                                                                                                                                                                                                             15.0%; Score 342; DB 11; Length 4 25.8%; Pred. No. 5.4e-22; Live 52; Mismatches 166; Indels
                                                                                                                              5 -> T.

F -> I.

S -> F.

Y -> C.

6C51D2CF1C4626DF CRC64;
                 Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 HVNVTCIVNVCSSDHSSQCSSQASATVGDPDAKPSASP 403
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                                                                                                                                                                                                                                                                                                                                                                            ----DKTHTCP-----PCPAPELL----
         MEDLINE-95178848; PubMed-7873884;
                                                                             INTERPRO; IPR001368; -. PFAM; PF00020; TMRE_CG; 4. PROSTIE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                ог <u>г</u> о ≻
                                                                                                                                                                                  48686 MW;
                                               Mamm. Genome 5:726-727(1994).
EMBL: X76401; CAA53981.1; -.
HSSP; P19438; INCF.
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08,
15,
                                                                                                                                                                                                                                   Conservative
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345
421
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93
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93
268
345
421
459 AA;
                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                         Best Local Sim
Matches 103;
                                                                                                                                                                        VARIANT
SEQUENCE
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VARIANT
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 PERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSL-------ESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRIS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TNFR-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNFR-RELATED DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 HYDEETSHQLLCDKCPPGTYLKQHCT-----AKWKTVCAPCPDHYYTDSWHTSDECLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGLIALGLVNCFILVQRKKKPSCLQRDAKVPHV-PDEKSQDAVGLEQQHLLTTAPSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 AIPRTLYVSQPEPTRSQPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---FLFPPKPKDTLMISRTPEVTCVVVD--VSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a novel
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Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G., Vincenz C., Aggarwal B.B., Dixit V.M.;

"Identification and functional characterization of DR6, a nove domain-containing Thr receptor.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GGPSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 355
                                                                                                                                                                                                                                                                                                                                                                                              14.7%; Score 335; DB 11; Length 4 25.7%; Pred. No. 2.3e-21; cive 49; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parker A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                      -; 1.
; 51106 MW; F6C15046B48FF83C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIDVTV----DKTHTCP-----PCPAPELL-----
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                                                                                                                                                               INTERPRO; IPR001368; -. PFAM; PF00020; INFR_c6; 4. PROSITE; PS00052; INFR_NGFR_1; 2. PROSITE; PS50050; INFR_NGFR_2; 3. PRODOM; PD000771; -; 1.
EMBL; Y14620; CAA74969.1; JOINED.
EMBL; Y14621; CAA74969.1; JOINED.
EMBL; Y14622; CAA74969.1; JOINED.
EMBL; Y14623; CAA74969.1; JOINED.
EMBL; Y14679; CAA74969.1; JOINED.
HSSP; P19438; INCE.
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Primates; C
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.79
Matches 105; Conservative
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Mismatches 138; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                   367 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%; Score 275.5; DB 1
llarity 26.3%; Pred. No. 5.8e-16;
Conservative 53; Mismatches 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                         01, Created)
01, Last seq
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Create O1-NOV-1996 (TrEMBLrel. 01, Last S 01-CT-2000 (TrEMBLrel. 15, Last NOVEL ANTIGEN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95183140; PubMed=7877689;
    35;
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75224 MW;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                            115 PERNTVCKRCPDGFFSNE-
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Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7801;
 96;
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Q90544;
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SIGNAL
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                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                             54 YRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPC 113
                                                                                                                                                                                                                                                                                                               67 KELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD 126
                                                                                                                                                                                                                                                                                                                                GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS---GNSESTQKCGIDVTVDKT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                       223 -----PSP----GTAIF---PRP-EHMETHEVPSSTYVPKGMNSTESNSSASVRPKV-L 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 SSIQEGTVPDNTSSARGKEDVNKT -- LPNLQVVNHQ --- QGPHHRHIL -- KLLPSMEATG 320
                                                                                                                                                                                                                                   Gaps
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174 GTFSDVPSSVMKCKAYTDCLSQNLVVIRPGTKETDNVCGTLPSFSSSTS-----
                                                                                                                                                                                                                                                           7 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC
                                                                                                                                                                                                                                                                                                                                                                                                                        184 HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED-----PEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Zheng S., Cao J., Cao W., Cai X., Geng L.;

Identification and characterization of SNC73, a gene which is regulated in colorectal cancer.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, PARO67427, PAR.

INTERPRO; IPR003006;
                                                                                                                                                                                                                                   48;
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                                                                                                                                                                                                        Length 655;
                                                                                                                                                                                                                                44; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00047; 19; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 384 AA; 40947 MW; BA7ADC3CA5A9DD48 CRC64;
                                                                                                                                                              655 AA; 71844 MW; 48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                       12.9%; Score 294; DB 4; 27.8%; Pred. No. 1.3e-17;
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                                                               PFAM: PF00020; TNFR_G5; 4.

PFAM: PF00531; death; 1.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS50017; DEATH_DOMIN; 1.

PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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28.2%;
EMBL; AF068868; AAC34583.1;
EMBL; AL096801; CAB75692.1;
HSSP; P07174; 1NGR.
INTERPRO; IPRO00488; -.
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                                                                                                                                                                                                                                87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                   PRODOM; PD000771; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 -EKTISKAKGQPR 304
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Best Local Similarity
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                                                                                                                                                 Receptor.
SEQUENCE
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Best Local S
Matches 87,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 PSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 PPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAV 325
                                                                 --TSSKAPCRKHTNCSVFGLLLTQK 155
                                                                                                                                                                                                                                                               108 -----CLAGKSVT--CHVKHYTNPSQDVTV-----PCPVPSTPPTPSPST-PPTP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 DSWHTSDECLYCS-----PVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 LPPSPEEIQSTSSATLTCLIR --- GEYPDKVSVSWQKDDVSVSANVTNFPTALEQ -- DLT 409
                                                                                                                                                                                             156 GNATHDNICSGNSESTOKCGI-----DVTVDKTHTCPPCPAPELLGGPSVFLFPPKP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 HDNICSGNSESTQ-KCGIDVTVDKTHTCPP-------CPAPELLGGPSVFLF 203
                                                                                                                            49 PDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQ~ 107
71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostoma
                                                                                                                                                                                                                                                                                                                                208 K------DILMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 684;
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2FF9D2071CDA6DFD CRC64;
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CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC---KELQYVKQEC 76
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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FSTRSLLNLTAVEWRSGAKYTCTASH--PPSQSTVKRVIRNQKVDCRQTDI----SVSLL 463
                                                                                                                                NQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 379
                                                                                                                                            NCSVFGLLLTQKGNATHDNICSGNSESTQKCGI-----DVTVDKTHTCPPCPAPELL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TSSKAPCRKHT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSESGQNVTARNFPPSQDASGDLYT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The European IMAGE consortium for integrated Molecular analysis of
                                                 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRDEL-TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 TSSQLTLPATQ-----PCPDGKSVT--CHVKHYTNPSQDVTV-----PCPVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 GGPSVFLFPPKP-----KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PPPPCCHPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGATFTWTPSSGK
                                   PPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNSTYRV
                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Κ.,
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
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                                                                                                                                                                                                                                                                                                                                                                                                        Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389978; CAB97534.1;
NON TER
SEQUENCE 416 AA; 44786 MW; 8C41708BBBAB4687 CRC64;
                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Estivill X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%; Score 273.5; DB 4; ilarity 27.5%; Pred. No. 4.8e-16; Conservative 37; Mismatches 137;
                                                                                                                                                                                                                                                                                                                        HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                              416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPGFGVVQAGTPERNTVCKRC-PDGFFSNE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Auffray C., Ansorge W., Ballabio A.,
Lehrach H., Poustka A., Lundeberg J.;
                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                           :|| | | :|: | | || 640 DITYSCLVGHPSLNRDLIRSTNKS 663
                                                                                                                                                                            380 GNVFSCSVMHEALHN---HYTQKS 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                        IMMUNOGLOBULIN
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                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and dendritic-cell function.";

stutes 390:175-179(1997).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AF019046; AAB86810.1;
-- HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · · · ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'A homologue of the TNF receptor and its ligand enhance T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Mismatches 147; Indels 119;
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                                                                                                                                                                                                                                                                                                                                                                                               Dougall W.C.,
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-LIVER REITHELIUM;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.
Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
349 SQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
W. LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
W. FRCIBYZE99511DBE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 253.5; DB 1.
24.9%; Pred. No. 4.4e-14;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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PROSITE: PS00625; TNFR_NGFR_1; UNKNOWN_1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
PROSITE: PS01050; TNFR_NGFR_2; 1.
                                                                                                                                               Created)
                                                                                                            PRT;
                                                                                                                                                                                                                  INDUCED CYTOKINE RECEPTOR) (RANK).
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INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
                                                                                                                                             (TrEMBLrel. 05,
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                                                                                                            PRELIMINARY;
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                     TNFRSF11A OR RANK.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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154
35
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                                                                                                                                                            01-JAN-1998
01-OCT-2000
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SIGNAL
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CARBOHYD
SEQUENCE
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Search completed: March 1, 2001, 09:20:09 Job time: 407 sec

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 (without alignments)
 320.024 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-389-782A-6 2274 1 ETFPPKYLHYDEBTSHQLLC......VMHBALHNHYTQKSLSLSPG 406

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

88757 seqs, 32294092 residues

Searched:

88757 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01857 homo	homod	homod	homod	oryct	52	mus mu	37	P20761 rattus norv	P20759 rattus norv	P01868 mus musculu	P01869 mus musculu	P20762 rattus norv	P01863 mus musculu	P01865 mus musculu	P01864 mus musculu	P20760 rattus norv	P01866 mus musculu	P01867 mus musculu	P06336 mus musculu	homo	1 homo	ratto	mus m	P01854 homo sapien		- 60		P04221 oryctolagus	P25119 mus musculu	P01874 canis famil	m	P20768 suncus muri
SUMMARIES	. 01	GC1_HUMAN	GC2_HUMAN	GC4_HUMAN	GC3_HUMAN	GC_RABIT	GC2_CAVPO	GC3_MOUSE	GC3M_MOUSE	GCB_RAT	GC1_RAT	GC1_MOUSE	GCIM_MOUSE	GCC_RAT	GCAA_MOUSE	GCAM_MOUSE	GCAB_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	EPC_MOUSE	MUCB_HUMAN	MUC_HUMAN	EPC_RAT	MUC_MOUSE	EPC_HUMAN	MUCM_MOUSE	MUC_RABIT	TNR2_HUMAN	MUCM_RABIT	TNR2_MOUSE	MUC_CANFA	MUC_MESAU	MUC_SUNMU
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. •	Query Match		50.5	50.1	49.9	40.3	39.4	37.3	37.0	36.7	35.9	35.7		S	5.	35.4	S.	4		4	9	15.9					•			•	•	•	14.5	14.5
	Score	123	1148	1138.5	1134.5	917	895.5	848.5	842.5	834	817.5	812.5	812.5	802	804	804	797	782	779.5	779.5	366.5	361.5	359	355.5	354	352	349	346.5	345.5	341.5	337	335.5	330.5	329.5
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P23085 heterodontu	_										P25942 homo sapien	
HVC2_HETFR	HVCS_HETFR	ALC_RABIT	MUC_CHICK	HVCM_HETFR	CD40_MOUSE	HVC3_HETFR	ALC1_HUMAN	ALC1_GORGO	HVC1_HETFR	ALC2_HUMAN	CD40_HUMAN	
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438	438	299	446	461	289	393	353	353	370	340	277	
13.6	13.0	13.0	12.9	12.8	12.8	12.5	12.2	12.2	12.2	12.0	11.6	
308.5	296	295	292.5	292	291.5	285	277.5	276.5	276.5	273.5	264	
34	32	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

RESULT SCI_HUMAN LD GOLD DT 21-JUMAN LD GOLD DT 21-JUMAN LD GOLD LD GO
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                                                                                                                                                                                                                                      entities requires a license@lsb-sib.ch).
                                                                                                                                                             RESIDUES
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                                                                                      Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal 1961 immunoqlobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
[8]
                                                                                                                                                                                 MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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K -> K (IN GLM(3) MARKER).
/FIId-VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FIId-VAR_03887.
L -> M (IN GLM(NON-1) MARKER).
/FTIG-VAR_03888.
REMOVED POST-TRANSLATIONALLY.
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MEDLINE-81208100; Pubmed=7236608;
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HINGE.
CH2.
                                                                                                                                                                                                                                                            EMBL; J00228; AAC82527.1; ALT_INIT.
Biochemistry 9:3188-3196(1970)
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0; ig_MHC; 2.
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                                                                                                                                                                                                                                                                                     MIM; 147100; -
INTERPRO; IPRO00495; -.
INTERPRO; IPRO03006; -.
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1FC2; 15-JUL-92.
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PROSITE; PS00290;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1231; DB 1; Length 330;
Pred. No. 2.9e-76;
3; Mismatches 12; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2 CHAIN C'REGION.
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MEDLINE=82197621; Pubmed=6804948;
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92.58;
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330 AA;
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Matches 233; Conserv
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INTERCHAIN (WITH A HEAVY CHAIN)

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INTERPRO; IPR000495; -.
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P01861;
                          DISULFID
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SEQUENCE
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                                                                                                                                                                                                                MEDLINE-80001357; PubMed-113060; Connell G.E., Parr D.M., Hofmann T.; "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein."; Can. J. Biochem. 57:758-767(1979).
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Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri
'Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 238-275 (ZIE).
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Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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                                                                        "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
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Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
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Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 25; 59; 60 AND 264-268 (ZIE)
SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
                                                    Wang A.-C., Tung E., Fudenberg H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH1.
HINGE.
CH2.
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                          MEDLINE=81007873; PubMed=6774012
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PROSITE; PS00290; IG_MHC; 2.
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/FTIG=VAR_003889.
AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE).
8310878C6878CF9C CRC64;
                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                Length 326;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                Score 1148; DB 1;
Pred. No. 1.1e-70;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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326 RE
35884 MW;
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87.0%;
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SEQUENCE OF 1-30 AND 81-326.
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326
326 AA;
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Best Local Similarity
Matches 215; Conserv
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CARBOHYD
MOD_RES
VARIANT
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MEDILINE-81021548; PubMed-6774747;
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"Primary structure of human gamma 3 immunoglobulin deletion mutant:
"Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human 1gG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                             45;
                                                                                                                                                           50.1%; Score 1138.5; DB 1; Length 327; 71.1%; Pred. No. 4.8e-70;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC)
                                                                                                (WITH A HEAVY CHAIN). (WITH A HEAVY CHAIN).
                                                                              INTERCHAIN (WITH A LIGHT CHAIN).
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                            Immunoglobulin C
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 2.
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                             domain;
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                                                                                                                                                                   Similarity
                            [mmunoglobulin
                                                                                                                                                                   Best Local Sim.
Matches 224;
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P01860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REF. 2.
MISCELLANBOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
AND ALL OF THE CHI REGION.
MISCELLANBOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
                                                                                                                                                                                                                                                                                                                                                                                        NORWALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELLANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                                                                                                                                                                                                 Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin B.C., Hood L., Buxbaum J.N.; Gamma Heavy chain disease in man: cDNA sequence supports partial gene deletion model.";
                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 79;3260-3264(1982).
-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
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                 MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; The amino acid sequence of 'heavy chain disease' protein zUC. Structure of the Fc fragment of immunoglobulin G3."; Blochem. Biophys. Res. Commun. 71:907-914(1976).
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DOMAIN 12 73 HINGE.
HINGE.
DOMAIN 74 183 CH3.
DOMAIN 184 289 CH3.
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REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN 2UC).
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                                                                                                                                                                        SEQUENCE FROM N.A. (DISEASE PROTEIN OMM)
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PIR; A02149; G3HUWI.
                                                                                                                                                                                               MEDLINE=82247835; PubMed=6808505
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PROSITE; PS00290; IG_MHC; 1.
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OV -> EB (IN ZUC). /FTId=VAR_003890.

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SEQUENCE OF 132-161
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Best Local Similarity
Matches 169; Conserv
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-76135469; PubMed-1243651;
Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of :immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                            ; Score 1134.5; DB 1; Length 290; Pred. No. 7.8e-70; 19; Mismatches 25; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84030930; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the
                                                                                                       FTId=VAR_003896.
E69CBC95705B2F46 CRC64;
P -> L (IN OMM).
/FTId=VAR_003891.
F -> Y (IN OMM).
/FTId=VAR_003892.
T -> A (IN OMM).
/FTId=VAR_003893.
S -> N (IN OMM).
/FTId=VAR_003893.
                                                                           MISSING (IN ZUC).
/FTId=VAR_003895.
F -> Y (IN OMM).
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA CHAIN C REGION.
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69.0%;
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 134
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                      gamma genes
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                                                                                             MEDLINE-70110015; PubMed-5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
Sequence studies of the Fd section of the heavy chain of
immunodiohulin G.":
                                                                                                                                                                                                             SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.; (In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Stockholm (1967).
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E15 MARKER).
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"Heavy chain genes of rabbit IgG: isolation of a heavy chain and identification of two genomic C groc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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PROSITE; PS00290; IG_MHC; 1.
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
                                                                                                                                                                                                                                                                                                                                                            Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Blochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
253 ISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHY 312
                                                                                                                                                                                                                                                 SEQUENCE OF 4-68.
MEDLINE=71058471; PubMed=5538606;
Birshtein BY., Hussain Q.Z., Cebra J.J.;
Birshtein BY., Amino gid sequence of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-75036073; PubMed-4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Iracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig 1gG2
                                                                                                                                                                          Euteleostomi;
                                                                                                                             21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G GAMMA-2 CHAIN C REGION.
Cavia porcellus (Ginnea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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HEAVY CHAIN).
HEAVY CHAIN).
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NON_TER
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MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-75036072; PubMed-4429665;
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                STANDARD;
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INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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79
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107
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                     TOKSLSLSPG 406
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TOKSISRSPG 322
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SEQUENCE OF 1-3.
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                                                                                                                                                                                                                                                                   IRTP 100
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                                                                                                                                                                       Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE-85627161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                61 GLYSLTSMVTVPSSQKATC-----NVAHP-----ASSTK---VDKTVE
                                                                                                                                                                                                                                                                                                               ----TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                        DB 1; Length 329
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                                                   5D231B7164D1FBA9 CRC64;
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Immunoglobulin C region; Glycoprotein; Transmembrane;
Alternative splicing.
  N-LINKED (GLCNAC. . .).
                                                                                                                      Score 895.5; DB 1;
Pred. No. 1.1e-53;
31; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329
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178 N-
308
36074 MW;
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36228 MW;
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59.98;
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Matches 173; Conservative
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INTERPRO; IPR000495; -.
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248
329 AA;
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224
329 AA;
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P22436;
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                                                                               107 FGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSG 166
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                                                                                                                                                                                                                                                                                                                          NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 344
                                            Gaps
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                       YGALSSGV---RTVSSVLQSGFYSLSSLVTVPSSTWPSQTVI------CNVAHP---AS
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MEDLINE-85027161; Pubmed-6092053;
Wels J.A. Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1963 constant region gene.";
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MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
Length 329;
                                            Indels
  Score 848.5; DB 1;
Pred. No. 1.6e-50;
                                            75;
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15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
Mus musculus (Mouse).
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                                         47; Mismatches
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EMBL; V01526; CAA24767.1; ALT_SEQ.
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Mammalia; Eutheria; Rodentia;
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PROSITE; PS00290; IG_MHC; 1.
37.3%;
54.0%;
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                                         Matches 163; Conservative
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                       Similarity
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P03987;
  Query Match
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Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
PIR; PSO018; PSO018.
INTERPRO; IPRO00495; -.
INTERPRO; IPRO03006; -.
                                                                                                                                                                                                                                                                                                                                                                                           107 FGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSG 166
                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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CH1.
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CH2.
CH3.
POTENTIAL.
CYOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> F (IN REF. 2).
E -> F (IN REF. 2).
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                                                                                                                                                                                                                       37.0%; Score 842.5; DB 53.8%; Pred. No. 5e-50; iive 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 GAMMA-2B CHAIN C REGION.
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MEDLINE-89232738; PubMed=3149946;
                                                                                                                                                                   MM;
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                       Query Match 37.0%
Best Local Similarity 53.8%
Matches 162; Conservative
                                                                                                                                                                   43929
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NON_TER 1 15 15
DISULFID 27 80
DISULFID 106 106
DISULFID 109 109
DISULFID 112 112
DISULFID 1147 207
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388
398 AA;
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PIR; PS0017; PS0017.
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                                                                                                                                                                                                                      AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 358
                                                                                                                                                                                                                                 225 PKGLVRKPQVYVMGPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVM 284
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                   VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
                                                                                                                                -----TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
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                                                                                      130 SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKTH--
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                                           Length 333;
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                                           Score 834; DB 1;
Pred. No. 1.5e-49;
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JUL-1999 (Rel. 38, Last annotation update)
GAMMA-1 CHAIN C REGION.
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                                                                41; Mismatches
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55.6%;
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                                                     Best_Local Similarity 55.6
Matches 160; Conservative
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15-JUL-1999
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SEQUENCE
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Indels

37;

Similarity 60.5%

Matches 144;

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172 QKCGIDVTVDKTHTCPPCPAPELLGG----PSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 228

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100 RNCGGD------CKPC----ICTGSEVSSVFIFPPRFKDVLTITLTPKVTCVVVDISQ 147
                                                                                                                                    PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 348
                                                                                                                                                                                                                                                                         SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDILE-80012837, PubMed-113776,
REGGERS J., Clarke P., Salser M.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki. Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                           349 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                     EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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(Rel. 01, Last sequence update)
(Rel. 39, Last annotation update)
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J. Biol. Chem. 253:6068-6075(1978)
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MEDLINE=73008889; PubMed=5073237;
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30-MAY-2000 (
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P01868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                PFAM; PF00047; 1g; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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                                                                                                                                                INTERCHAIN (WITH A LIGHT CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                      281 YEVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
                                                                                                          CH1.
HINGE.
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SEQUENCE OF 323-393 FROM N.A.
 V00793; CAA24173.1; -. V00793; CAA24174.1; -. V00793; CAA24175.1; -. V00795; CAA24176.1; -.
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62.3%;
CAA24173.1;
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                                       MGD; MGI:96446; Igh-4.
INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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                                                                                          Alternative splicing.
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Best Local Similarity
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                                PIR; A02159; G1MS
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ID GC1M_MOUSE
AC P01869;
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MEDLINE-8222190; PubMed-6283537;
MEDLINE-8222190; PubMed-6283537;
Muslectide sequences of yene segments encoding membrane domains of immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
Froc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
IN SPRCIES FOR IG GAMMA CHAINS. THES MEMBRANE-BOUND IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
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MEDLINE-82197626; PubMed-6804950;
TYler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O. "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28 residue intracellular conserved transmembrane sequence and a 28 residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain, Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane.
                                                                                                                                                                                                SEQUENCE OF 323-366 FROM N.A.
MEDILIDE-82115255; PubMed-6799207;
KROGETS J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN)
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                                                                                                                                                                                                                                                                                                                         "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
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62.3%; Pred. No. 5.1e-48;
tive 44; Mismatches 35;
                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A, 79:2008-2012(1982).
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HINGE.
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
PIR; B00159; GIMSM.
MGD; MGI:96446; IGH-4.
INTERPRO; IPR000495; --
INTERPRO; IPR000405; --
PPAM; PF00047; 19; 3.
PROSITE; PS00299; IG_MHC; 1.
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340
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393 AA;
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Matches 139; Conserv
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274 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=6787604;
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MEDLINE=74175517; PubMed=4831970;
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                                                                                                                                                             STANDARD;
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NHHTQKNLSRSPG
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SEQUENCE FROM N.A.
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P01863;
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GCAA_MOUSE
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                                                     VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 303
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                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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           REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
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                                                                                                                                                                                                                                                                           MEDLINE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemann en a rat immunoglobulin gamma 2c heavy chain constant
"Sequence ODNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5FCD7B7933850773 CRC64;
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                                                                                              YEVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
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Pred. No. 1.4e-47;
1; Mismatches 49;
                                                                                  FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
GADMA-2C CHAIN C REGION.
Rattus norvegicus (Rat).
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HINGE.
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PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                            STANDARD;
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113
143
249
329 AA;
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SEQUENCE FROM N.A.
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Best Local Simi
Matches 146;
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                                                                                                                                                                                 MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sikorav J.-L., Auffray C., Rougeon F.; "Structure of the constant and 3' untranslated regions of the Balb/c gamma 2a heavy chain messenger RNA."; Nucleic Acids Res. 8:3143-3155(1980).
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de Preval C., Fougerau M.;
de Preval C., Fougerau M.;
immunotion of the primary structure of a mouse gamma G2
immunoglobulin. Identification of the disulfide bridges.";
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30-WL-1986 (Rel. 01, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-2A CHAIN C REGION, A ALLELE.
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                  EMBL; J00471; AAB59661.1; ALT_INIT
                                                                       INTERPRO; IPRUUJOUU,
PFAM; PF00047; 19; 3.
PFAM; — PC00290; IG_MHC; 1.
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                                  PIR; A02154; G2MSAM
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Matches 145; Conserv
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunogolbolini gamma chains."

Proc. Natl. Acad. Sci. U.S., 79:2623-2627(1982).

-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAWMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' ENC. ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                        304 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 363
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                        5;
                                                                                                                         HEAVY CHAIN).
HEAVY CHAIN).
                                                                                              INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                        Length 330;
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15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
                                                                                                                                                                                                                                                                       Score 804; DB 1;
Pred. No. 1.6e-47;
                                                               Immunoglobulin C region.
                                                                                                                                                                                                                                                             35.4%; Scc. 65.0%; Pred. No. ... 30; Mismatches
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P01865;
21-JUL-1986 (Rel. 01, Created)
                             PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                          36389
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INTERPRO; IPR000495; -.
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82
107
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107 CPPCKCPAPULLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE 166 244 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 303 REPOVITLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS YFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG Search completed: March 1, 2001, 09:17:47 Job time: 265 sec 227 364 304 287

ij

Gaps

5;

46;

35.4%; Score 804; DB 1; 65.0%; Pred. No. 1.9e-47; tive 30; Mismatches 46;

Conservative

Length 399; Indels

AL)

N-LINKED (GLCNAC. . ) (POTENT 4C38138BFAED3FF0 CRC64;

W.

44020

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).

**444** 

INTERCHAIN (WITH INTERCHAIN (WITH INTERCHAIN (WITH

INTERCHAIN (WITH A LIGHT CHAIN)

Alternative splicing.

MGI:96443; IGH-1.

186 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE

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MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.

SEGMENT OF MU CHAINS

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 1, 2001, 09:15:46; Search time 79.26 Seconds
(without alignments)
347.813 Million cell updates/sec

Title:

US-09-389-782A-6

Perfect score:
2274
Sequence:
1 ETFPPRXLHYDEETSHQLLC......VMHEALHNHYTQKSLSLSPG 406
Scoring table:
Gapop 10.0, Gapext 0.5
Searched: 195891 seqs, 67900655 residues
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: PIR_66:*
1: pir1:*
2: pir2:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq qamma-1 chain C	Ig gamma-1 chain C	Ig heavy chain V r	Ig heavy chain V r	Ig gamma chain C r	Ig gamma-3 chain C	Ig gamma-3 chain C	Ig gamma-2 chain C	Ig gamma-4 chain C	Ig gamma-3 heavy c		Ig gamma 2b chain	Ig gamma 2a chain	Ig gamma 4 chain c	Ig gamma-2 chain C	Ig gamma 1 chain c	Ig gamma 3 chain c	Ig heavy chain pre	Ig gamma-3 chain C	Ig gamma-3 chain C	Ig heavy chain C r	Ig gamma-1 chain -	Ig gamma-2b chain	monoclonal antibod	Ig gamma-1 chain C	ф		b	g gamma-2a
SUMMARIES	QI	СННО	S31866	S72664	869339	PT0207	A23511	A60764	G2HU	G4HU	G3HUWI	GHRB	147160	147159	147162	·G2GP	147158	147161	S22080	G3MSC	G3MSM	C30554	S31459	PS0018	PC4436	PS0017	G1MS ·	G1MSM	S00847	G2MSA
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æ	Query Match	4	₹	4	53.8	~	0	0	50.5		ď.	40.3	39.8	σ	39.8	o.	39.5	œ	37.8	7	7	37.0	37.0		36.2	35.9	35.7	35.7		35.4
	Score		1228	1227	1222.5	1180	1156	1154	1148	1138.5	1134.5	917	907	907	905	895.5	891.5	819	858.5	848.5	842.5	841	841	834	822.5	817.5	$\sim$	812.5	802	804
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Ig gamma-2a chain	Ig gamma-2b chain	Iq qamma-2b chain	Iq qamma-2b chain	Iq qamma-2 chain C	Ig gamma-2b chain	Ig gamma heavy cha	Ig heavy chain V-I	Ig heavy chain VHI	Iq qamma-1 chain C	Iq Y heavy chain (	Ig heavy chain pre				
G2MSAM	S37483	G2MSAB	S40295	PS0019	G2MS11	G2MSBM	S25057	806611	S01321	I46732	A36040	S69340	S14236	B46529	S04845
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399	469	335	446	322	336	405	474	327	475	180	218	249	152	572	549
35.4	35.4	35.0	34.9	34.4	34.3	34.3	34.3	33,5	33.3	30.9	25.3	25.2	24.9	17.3	16.3
804	804	797	794	782	779.5	779.5	779.5	761	757.5	702	574.5	572.5	266	394.5	371
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

195891

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Gaps

88

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cloned gene produc
                                    lchia coli
May-2000
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C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S72664
B;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
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                           A, Note: Homo sapiens (man) gene engineered and expressed in Escheric C, Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 15 C, Accession: S31866

R; Filpulo: Sand C, A, Sand C, Sand C,
                                                                                                                                                                                                             February 1993
protein-protein interactions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:
KFGYWORDS: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1.37 < KKHA>
A; CSCOSS-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1228; DB 4;
Pred. No. 9.1e-69;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1227; DB 2;
Pred. No. 1.6e-68;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S72664
Ig heavy chain V region precursor - human
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100.0%; Pre
0; /
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Best Local Similarity 91.2%;
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
C; Species: synthetic
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Best Local Simi
Matches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156
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A; Wolecule type: protein
A; Nolecule type: protein
A; Nolecule type: protein
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565; MUID:71064027
A; Contents: annotation; disulfide bonds
B; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
B; Protein: Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Reference number: A91667; MUID:77070267
A; Contents: annotation; disulfide bonds
A; Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; cene.

A; cene.

A; Map position: 14q32.33-14q32.33

A; Map position: 14q32.33-14q32.33

A; Introns: 99/1; 114/1; 224/1

A; Introns: 99/1; 114/1; 224/1

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Reywords: duplication; 91; coprotein; heterotetramer; immunoglobulin

F; 20-85/Domain: immunoglobulin homology < IM2>
F; 213-206/Domain: immunoglobulin homology < IM3>
F; 243-310/Domain: immun
                                                                                                                                                                                                                                                                                                                                                                                           KOI
                                                                                                                                                           A; Molecule type: protein
A; Molecule type: protein
A; Residues: 11-34, (2, 7, 56-96, KK, 98-115, 02, 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E',
A; Note: this sequence has the Glm(17) and Glm(1) markers
B; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seylar: 8 2. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins 1961 R
A; Reference number: A91723; MUID: 83289131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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F;103/Disulfide bonds: interchain (to light chain) *status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) *status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THDNICSGNSE-STQKCGIDV---TVDKTHTCPPCPAPELLGGPSVFLFPPKPTLMIS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLTVLHQDWL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1231; DB 1;
Pred. No. 7.8e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: myeloma protein KOL; disulfide bonds A; Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                      MUID:77070269
Nie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-1 chain C region - synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.18; 92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.1
Best Local Similarity 92.5
Matches 233; Conservative
                                A; Reference number: A91668;
A; Contents: myeloma protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYTQKSLSLSPG 406
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                                                                                                                  B91668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: IGHG1
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c5, u) with an IGHG4 conv
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R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Accession: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma-3 chain C region, form LAT : human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Apecies: Homo Sapiens (man)
C;Accession: A60764
R;Huck, S; Lefranc, G.; Lefranc, M.P.:
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IA;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                           23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 NSESTQKCGIDVTVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 PENNYNTTPPMLDSDGSFFLYSKLIYUNGKSRWQQGNIFSCSWMHEALHNRFTQKSLSLSPG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 VQAGTPERNT--VCKRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNICSG 166
                                                                                                        ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 VELKTPLGDTTHTCPRCPEP-KSCDTPPPCPRCPEPKSCD---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHEDDEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 377;
                                                                                                                                                                                                                                                                                                                                                                    Ig gamma-3 chain C region (allotype G3m(b)) - human
C.Species: Homo sapiens (man)
C.Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                195 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234
                                                                                                                                                                                  361 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.8%; Score 1156; DB 2; 74.3%; Pred. No. 3.6e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.8%
Best Local Similarity 74.3%
Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A60764
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: GDB:IGHG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347
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                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C.Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C.C.Dates 19-War-1997 #sequence_revision 19-Mar-1993
R.Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Blochem. 229, 54-60, 1995
A.F.Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A.R.Reference number: S69339; MUID:95262687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma chain C region - chimpanzee C;Species: Pan troglodytes (chimpanzee) C;Species: Pan troglodytes (chimpanzee) C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999 C;Accession: PTC207 R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L. Mol. Immunol. 28, 319-322, 1991 A;Fitle: Nucleotide sequence of chimpanzee Fc and hinge regions. A;Reference number: PTC207; MUID:91287716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 347
303 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GIDVTV-----DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin F;48-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1222.5; DB 2; Leusens
Pred. No. 2.9e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%; Score 1180; DB 2; 98.6%; Pred. No. 7.3e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                   Ig heavy chain V region precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.8%;
95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 98.69
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 95.4 Matches 228; Conservative
                                                 396 YTOKSLSLSPG 406
                                                                               363 YTOKSLSLSPG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-234 <EHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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02-Apr-1982 #text_change 16-Jul-1999
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F;20-85/Domain: immunoglobulin homology <IMD>
F;239-306/Domain: immunoglobulin homology <IMD>
F;239-306/Domain: immunoglobulin homology <IMD>
F;279-81,14/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #s;102,103;106,109/Disulfide bonds: interchain (to heavy chain) #s;102,103;106,109/Disulfide bonds: interchain (to heavy chain) #s;105,103;106,109/Disulfide bonds: interchain (to heavy chain) #s;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,103;105,1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1148; DB 1; Length 326;
Pred. No. 9.6e-64;
9; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin C-gamma4
   R;Hofmann, T.; Parr, D.M. submitted to the Atlas, March 1980 A;Reference number: A9459, A;Reference number: A9459, A;Contents: annotation; Zie, revisions to residues 25, 59, 60, A;Note: the revised sequence differs from that shown in having
                                                                                                                                                                                   Rimilstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immu A;Title: Disulphide bridges of the heavy chain of human immu A;Reference number: A90253; MIID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-146, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-327 < ELL>
A; Note: the sequence was determined from the germline gene
R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:119338; OMIM:147110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nuclectide sequence of a human im
A;Reference number: A90933; MUID:83157104
A;Accession: A90933
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Best Local Similarity 87.0
Matches 215; Conservative
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A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con A;Reference number: A93906; MUID:82197621
A;Accession: A93906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: The amino acid sequences of the three heavy chain constant region domains of a A,Reference number: A90752; MUID:80001357
A,Contents: myeloma protein Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'222',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin A;Reference number: A93132; MUID:80114419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: Lys-326 is probably removed posttranslationally
R; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an A; Rochents: myeloma protein Til
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C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSESTQKCGIDVTVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 226
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
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                                                                                                                                                                                                                    Length 377;
A;Molecule type: DNA
A;Residues: 1-377 <HUC.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
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A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                           Score 1154; DB 2;
Pred. No. 4.8e-64;
6; Mismatches 37
                             ,16;
                                                                                                                                                                                                                    50.7%;
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. 16, 923-925, 1979
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A; Residues: 238-275 <HOF>
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Best Local Similarity
Matches 223; Conserv
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A;Teference number: A90442; MUD:81021548
A;Contents: heavy chain disease protein Wis
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 cFRA>
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A;Note: the sequence of residues 42-76 was taken from the reference that follows
B;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
                                                                                                                                                   A;Gene: GDB:1GHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:119340; 21/1
C;Complex: An immunoq1obulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoq1obulin C region; immunoq1obulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>
                       Partial amino acid sequence of the constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                 F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:240-307/Domain: immunoglobulin homology <IM3>
F:244/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Homo sapiens (man)
C; Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C; Accession: A0042; A9219; A90198; A93915; A02149
E; Frangione, B.; Rosenwaser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma-3 heavy chain disease proteins - human
              A; Reference number: A90249; MUID:70207560 A; Accession: A90249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 LHNHYTQKSLSLSLG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 APCRKHTN----CSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 LHNHYTQKSLSLSPG 406
                                                                                        A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
Biochem. J. 117, 33-47, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                     C; Genetics
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A; Molecule type: protein
A; Residues: 59-125, EB',128-226,228-289 <WOL>
A; Molecule type: protein lacks most of the V region, all of the CH1 region, and part of t R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, Proc. Natl. Acad. Sci. US.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti A; Reference number: A93915; MUID:82247835
A; Contents: heavy chain disease protein Omm
A; Recession: A93915
A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125, E',127-133, 'L',135-136, 'E',138, 'Y',140-154, 'D',156-A; Note: a carboxyl-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu A; Accession: A90198
                                                                                                                                            A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other
                                                                                                                                                                                                                                                                                             69, and 72 form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
A;Title: Primary structure of the 'hinge' region of human 1gG3. Probable quadruj
A;Reference number: A92219; MUID:77118561
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of j
A;Accession: A92219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid F;203-270/Domain: immunoglobulin homology <IMM>F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimenta. F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 PSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVWHEALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
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                                                                                                                                                                                                                                                                                                                                                                                                           protein ZUC.
                                                                                                                                                                                                                                                                                  A;Note: cystelles at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein A;Reference number: A90198; WUID:77021516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 CLKHRSC---PPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma chain C region - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
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Matches 216; Conservative
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rbu Mar

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Id7160

Ig gamma 2b chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: Id7160

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: Id7158; MUID:95015845

A;Accession: Id7160
                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PI$:g433126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF&CSVM 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGNSESTOKCGID-----VTVDK---THTCPPCP-----APELLGGPSVFLFPHRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: 19G2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.9%; Score 907; DB 2; Length 32
65.9%; Pred. No. 6.1e-49;
ive 33; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 HEALHNHYTQKSISKTPG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity 65.99
Matches 170; Conservative
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A; Residues: 1-328 <KAC>
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Best Local Simi
Matches 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: protein
A.Residues: 1-47, E', 49-71, PV', 72-128 < PRA>
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, M.; Hood, L.; Knight, K.L.
A.Reference number: A93928; MUID:83299917
A.Reference number: A93928
A.Reference number: A93928
A.Residues: 88-103, M., 105-143, E', 145-184, A', 186, E', 188-266 < MAR>
A.Residues: 88-103, M', 105-143, E', 145-184, A', 186, E', 188-266 < MAR>
A.Residues: Ba-103, M', 105-143, E', 145-184, A', 186, E', 188-266 < MAR>
A.Residues: Ba-103, M', 105-143, E', 145-184, A', 186, E', 188-266 < MAR>
A.Residues: Ba-103, M', 105-143, E', 145-184, A', 186, E', 188-266 < MAR>
A.Residues: R-116, 249-259, 1970
A.Title: Sequence has the full allotypic marker, 104-Met, and the e15 allotypic marker allother: A116, 249-259, 1970
A.Title: Sequence studies of the FG section of the heavy chain of rabbit immunoglobulin A.Reference number: A90245; MUID: 70110015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', A; Molec: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamally: immunoglobulin C region; immunoglobulin homology
C; Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E; 20-82/Domain; immunoglobulin homology < IMI>
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit 1gG heavy chain from the recombinant F-1 haplot A;Reference number: A91749; MUID:84030930
                                                                                                                                                                                                                                                                             the e14 marker, 185-Thr
                                                                                                                                                                                                                                                                                                                                                                the Fd sections of rabbit immunoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 132-143, 'E', 145-161 <FRU>
R; Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
R; Mamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A; Reference number: A94416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVF1FPPKPKDTLMISRT 132
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F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-323 < BER>
A; Note: this sequence has the d12 allotypic marker, 104-Thr, and t
R; Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A; Title: Sequence studies on the constant region of the Fd section
A; Reference number: A90290; MUID:76135469
A; Accession: A90290
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Best Local Simi
Matches 169;
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5

Gaps

Length 328;

CLVK 330

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G;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
B;Kacskovics, I:; Sun, J:; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences can the commer: 147158; MUID:95015845
A;Reference number: 147158; MUID:95015845
A;Reference number: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.9%; Score 907; DB 2; 65.9%; Pred. No. 6.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Mismatches
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A; Molecule type: protein
A; Residues: 134-226 <TRA>
R; Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A; Title: Primary structure of the C-H3 homology region from guinea pig 1gG2 antibodie
A; Reference number: A90385; MUID:75036073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Residues: 227-314 (TR2>
A) Residues: 227-314 (TR2>
A) Residues: 227-314 (TR2>
B) Coliveira, B.; Lamm, M.E.
B) Coliveira, B.; Millorifide bonds
A; Contents: annotation; disulfide bonds
A; Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
A; Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C; Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C; Complex: An immunoglobulin heteroteteramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin c region; immunoglobulin homoology
E; 21-81/Domain: immunoglobulin homoology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodie
A;Reference number: A90384; MUID:75036072
                                                                                                            A; Molecule type: protein
A; Residues: 1-3 <TRI>
R; Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A; Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A; Reference number: A90352; MUID:71058471
                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain from strain 13 guinea pig immunoglobulin-G(2). II.
MUID:71058486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKTH-- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GLYSLTSMVTVPSSQKATC-----NVAHP-----ASSTK---VDKTVEPIRTP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 2PBPCTCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 DNKPVGNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGQPREPQVYILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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59.9%; Pred. No. 3.1e-48;
iive 31; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                              A, Accession: A90352
A, Molecule type: protein
A, Residues: 4-68 ERIRA
Biochemistry 10, 9-17, 1971
A, Title: Structure of heavy chain
A, Reference number: A90359; MUID: 7, A, Molecule type: protein
A, Residues: 69-133,312-329 <TUR>
                         April 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.4% Best Local Similarity 59.9% Matches 173; Conservative
                   submitted to the Atlas, Apr
A; Reference number: A94553
A; Accession: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A90385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:9433129; PIDN:AAA52220.1; PID:9433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 SDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 392
                                   QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 330
                                                                                                                                                                                                                                                                                                                                                              GFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 388
                                                                                                                                                                                                                                                                                                                                                                                                 250 GFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQGGGIFQCAVM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274
                                                                                                                  211 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 SGNSESTQRCGID-----VTVDK---THTCPPCP-APELLG-GPSVFLFPPRPTLMIS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
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SGNSESTOKCGID-----VTVDK---THTCPPCP-----APELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putarive subclasses of swine IgG identified from the A;Reference number: I47158; MUID:95015845
A;Reference number: I47162
A;Reference number: I47162
A;Status; preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: immunoglobulin C region; immunoglobulin homology 82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 HEALHNHYTQKSISKTPG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 HEALHNHYTQKSLSLSPG 406
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147162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
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221 KGAPRMPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPI 280 Ωp

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Search completed: March 1, 2001, 09:15:48 Job time: 146 sec

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March 1, 2001, 09:17:03 ; Search time 70.93 Seconds
(without alignments)
195.724 Million cell updates/sec
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2274
1 ETFPPKYLHYDEETSHQLLC......VMHEALHNHYTQKSLSLSPG 406
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Copyright (c) 1993 --2000 Compugen Ltd.
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        268485 seqs, 34193795 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                       Title:
Perfect score:
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                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Fusion protein TNF	Sequence of a reco	Antiqenic peptide	Human Fas antigen	Plasmid pDC406/0x4	OX40/Fc mutein. C	Fusion protein of	Human neurturin re	Human NTNR alpha a	Rat neurturin rece	Rat NTNR alpha and	Integrin beta-1 ch
QI .	R24016	R51003	W60037	W50287	R81882	W48976	Y68949	W71603	Y80123	W71604	Y80124	W70540
DB	13	15	19	18	16	19	21	19	21	19	21	19
% Query Match Length DB ID	485	518	376	376	438	438	764	664	664	664	664	963
% Query Match	65.5	65.4	59.3	58.7	58.5	58.5	56.4	55.3	55.3	55.2	55.2	55.1
Score	1490	1487	1349	1334	1330	1330	1283	1257.5	1257.5	1254.5	1254.5	1253
Result	-	7	m	4	5	9	7	8	σ	10	11	12

	Y83136 Y83136 Y92207 W06683 Y44461 W860920 W18574 W18574 Y15123 Y23986 Y01037 Y01037 W96743 Y01037 Y01069 Y10869 Y10869	ALIGNMENTS  485 AA.  (1)  (2)  (2)  (3)  (485 AA.  (485	187. 837.
.00 3888 .00 5922 .00 502 .00 502 .00 502 .00 5022 .00 502 .00 502 .00 502 .00 502 .00 502 .00 502 .00 502 .00	3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3	1; Protein; first entry TNFRFC. s factor; TI Location/( 1.252 /note="1. 380.485 /note="1.	0120 4037 AG.
1250.5 1250.5 1250.1 1250 1247 1246.5 1244 1244	3 1241 54 1240 5 1241 54 12340 5 54 1238 5 5 54 1238 5 5 54 1234 54 1234 54 1233 5 6 1233 5 6 1233 5 6 1233 5 6 1233 5 6 1233 5 6 1233 5 6 1233 5 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 1233 5 6 6 6 1233 5 6 6 6 1233 5 6 6 6 1233 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	1 24016 standa 24016; 6-NOV-1992 usion protei umour necros ynthetic. ey egion egion egion	03-JUN-1992. 26-NOV-1991; 91EP- 28-NOV-1990; 90DE- (BEHW ) BEHRINGWERKE
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92US-0946236

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Treating TNF mediated inflammatory diseases with TNF antagonist esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis
                                                                                                                                                                                                                                                    Disclosure; Page 32-34; 47pp; English.
                                                                     14-SEP-1993; 0 93WO-US08666
                                                                                                                                           Smith CA;
                                                                                                                   (IMMV ) IMMUNEX CORP
                                                                                                                                                                    WPI; 1994-118172/14.
                                                                                                                                                                               N-PSDB; Q45225
                                                                                            15-SEP-1992;
                      WO9406476-A.
                                              31-MAR-1994
                                                                                                                                            Jacobs CA,
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                  The sequence is that of fusion protein TNFRFc comprising the extracellular domain of tumour necrosis factor (TNF) fused via a hinge region to the Fc part of the heavy chain of human 1gGl. It may be used as part of a cell free receptor binding test which can be used for the identification of agonists, antagonists, antibodies, biological activity of soluble cellular receptors, functional analysis of modified ligands and diagnostic or therapeutic substances.
                                                                                                                                                                                                                                                                                                                                                                                                                              163 pcapgtfsnttsstdicrphqicnvvai----pgnasmdavctstsptrsmapgavhlpg 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                 dqvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvck 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 pvstrsghtqptpepstapstsfllpmgpsppaedpeepksc-----dkthtcppcpap 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of a recombinant human (rhu) tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                              9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                Cell free receptor binding test contg. recombinant fusion protein comprising carrier bound to fusion partner coupled to fixed support, and second, labelled binding partner, for receptor or antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ESTQKCGIDVTVDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                          RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-------
                                                                                                                                                                                                                                                               Length 485;
                                                                                                                                                                                                                                                              ; Score 1490; DB 13;
; Pred. No. 3.6e-85;
17; Mismatches 75;
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                                                                                                                                                                                                                                                               65.5%;
                                                                                             Example; Fig 6; 24pp; German.
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           WPI; 1992-185084/23.
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Matches 292; Conserv
                                                                                                                                                                                                                            485 AA;
                                                                                                                                                                                                      See also R24017.
                                                                       screening etc
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                 Query Match
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O45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein waving a mol. wt. of about 75-80 kDa. The cloning of the cDNA for TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1 is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A crecombinant chinaric antibody may be produced having TNFR sequences substituted for the variable domains of either or both of the immunoglobulin molecule heavy and light chains and having missing control in given in Q45225/R51003. The run TNFR: C fusion gene was created by ligating the following fragments into a cloning vector: 1) an 867 bp Asp718-Pvuz fragment from pCAV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR. 2) a 700 bp Styl-Spel fragment from plasmid pIXX498 coding for 232 AAs of the CTC for ontg. the Fc fragment of human 1gGl. Plasmid pIXX498 is a yeast expression vector contg. the Fc fragment of human 1gGl. Plasmid pLiner Q45226, which encodes the 3' end of the truncated TNFR with the human 1gGl. S) and oligo linker, to finse the truncated TNFR with the human 1gGl. S) and oligo linker, c inker was created by PCR using primer Q45226, which encodes the 3' end of thuman 1gGl.

C 57-237 of human 1gGl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%; Score 1487; DB 15;
64.2%; Pred. No. 5.9e-85;
tive 19; Mismatches 84;
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Matches 289; Conservative
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Tumour necrosis factor receptor; chimeric antibody molecule;

immuglobulin,

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317

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377

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1..16
/label= sig_peptide
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/label= mat_peptide
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                                                                 15;
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                                                                 Conservative
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N-PSDB; V07004.
                                                  Similarity
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                                                                 270;
                                   Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart disease, ischemic restences of the heart, liver or kidney, and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This represents the antigenic peptide hFas (nd29) containing the Fc
                                                                                                                                                                                                                                                                                                                                                                heart failure; kidney failure; graft-versus-host disease; antibody; myocardial infarction; ischemic restenosis; endotoxic shock.
                                                ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "hFas antigen signal peptide"
                                                                                                                                                                                                                                                                                                                  Antigenic peptide hFas (nd29) containing Fc region.
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/note= "hFas (nd29) protein"
                                                                                                                           WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examples; Fig 5-9; 86pp; Japanese.
                                                                                                                                                                                                                     W60037 standard; Protein; 376 AA
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                                                                                                                                                                                                                                                                                   (first entry)
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31-OCT-1996;
27-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagata S,
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Peptide Protein

W60037;

RESULT W60037

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66 CKELQYVKQE--CNRTHNRVCECKEGRYLEIEFCLKHRSCPP----GFGVVQAGTPERNT 119
                                                                                                                                                                                                          120 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEÄTISKA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 359
                                                                                         LHYDEETSHQLLCDKCPPGTYLKQHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65
                                                                                                                Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV; apoptosis modulation; immunoglobulin G1 Fc; IgG1 Fc; fusion.
                                            62;
Length 376;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
Score 1349; DB 19
Pred. No. 1.5e-76;
5; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fas antigen derivative/IgG1 Fc fusion.
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23-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                      180 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239
                                                                                                                                                                                                                                                                                                                                                                                                                              DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                        KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cdeghgleveinctrtgntkcrckpnffcnstvc---ehcdpctkcehgiikectltsnt 134
                                                                                                                                                                                                                                                                 LHYDEETSHQLLCDKCPPGTYLKQHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65
                                                                                                                                                                                                                                                                            has low antigenicity, promotes apoptosis and is useful in treatment of viral and other diseases
                                                                  The present sequence is a Fas antigen derivative/IgG1 Fc fusion, which contains a Fas antigen extracellular region lacking one or more amino acid residues in the region from the amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted).

The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, es, diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                                                                                                                                                                                                                                VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT
                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                         Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pDC406/0X40/Fc* encoding an OX40/Fc mutein protein.
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell surface molecule; plasmid;
                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                    1.3e - 75
                                                                                                                                                                                                                                                                                                                                                                  kcke--egsrsnepks-----
                                                                                                                                                                                                                                  Pred. No. 1.3e
; Mismatches
                                                                                                                                                                                                                         Score 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pDC406/OX40/Fc*; membrane glycoprotein.
                                                Disclosure; Fig 4; 102pp; Japanese.
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                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R81882 standard; Protein; 438
                                                                                                                                                                                                                       58.7%;
65.6%;
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine;
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                            376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40; OX40-L;
                                                                                                                                                                                                                         Query Match
Best Local Simil
Matches 267; (
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                                                                                                                                                                                           Sequence
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crecqpghgmvnrcdhtrdtlchpcetgfyneavnydtckqctqcnh--rsgselkqnct 96
                                                                                                                                                                                                                                                                                                                                                                                                                                              This plasmid encodes an OX40/Fc antibody fragment mutein protein, and is used to express a soluble OX40/Fc mutein fusion protein for use in detecting CDNA clones encoding a OX40 ligand. The Fc fragment may be derived from human IgG1, and the plasmid may be used to transform the CV-1/EDNA (ATCC CRL 10478) monkey kidney cell line. Culture supernatant was purified by affinity chromatography and this was used, together with labeled goat anti-human IgG to screen various cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ptqdtvcrcr-----pgtqprqdsgyklgvdcvpcppghfs--pgnnq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elpstptlveprscdkthtcppcpapeaegapsvflfppkpkdtlmisrtpevtcvvvdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 438;
                                                                                                                                                                                                                                                                                                  New isolated DNA encoding the OX40 ligand polypeptide - als and host cells, used to produce recombinant ligand used in prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----ESTQKCGIDVTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.5%; Score 1330; DB 16
62.6%; Pred. No. 2.7e-75;
ive 23; Mismatches 80
                                                                                                                                                                   Goodwin RG;
                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Column 35-38; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą.
                                                                                                                                                                Gayle RB,
93US-0097827
                                                     93US-0097827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 263; Conservative
                                                                                                                                                                Fanslow WC,
                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                     WPI; 1995-357992/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA;
                                                                                                                                                                                                                                                  N-PSDB; T00829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OX40/Fc mutein.
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                                                                                                                                                                Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Shutter JR,
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                                                                                                                                                                                                                                                                                    Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                           Y68949;
                                                287
           227
                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgG1 antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The thin wentine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ptqdtvcrcr-----pgtqprqdsgyklgvdcvpcppghfs--pgnnq 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :| || : | || :| || :| || crecqpghgmvnrcdhtrdtlchpcetgfyneavnydtckqctqcnh--rsgselkqnct 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------DKTHTCPPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 elpstptlveprscdkthtcppcpapeaegapsvflfppkpkdtlmisrtpevtcvvvdv
                                                                                                                                                                                                                                                                                                                                                    Purified polypeptide OX-40 ligands - for co:stimulation of T-cell production and binding assays for OX-40 and homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 ackpwtnctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvgsttvwprts
                                                                                    'note= "Mutant Fc region of human IgG1 antibody"
                                                                                                         in
                                                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19; Length 438;
                                                                                                                                                                "changed from Gly in wild-type to Ala mutant"
                                                                                                         to Ala
                                                                "Extracellular domain of mouse OX40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----ESTQKCGIDVTV--
                                                                                                                                      ç
                                                                                                       /note= "changed from Leu in wild-type
                                                                                                                                    /note= "changed from Leu in wild-type
mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.5%; Score 1330; DB 19 62.6%; Pred. No. 2.7e-75;
                                                                                                                                                                                                                                                                                                      Goodwin RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Col 37-40; 26pp; English.
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                      Gayle RB,
                                                                                                                                                                                                                                   95US-0494574.
                                                                                                                                                                                                                                                               95US-0494574
                                                                                                                                                                                                                                                      93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263; Conservative
                                                                           ..438
                   - Homo sapiens.
- Mus sp.
                                                                /note=
                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                     Fanslow WC,
                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                        WPI; 1998-427099/36.
                                                                                                                                                      Misc-difference 228
                                                                                                                          Misc-difference 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AA;
                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                 N-PSDB; V32636.
                                                                                                                                                                                                                                  22-JUN-1995;
                                                                                                                                                                                                                                                               22-JUN-1995;
                                                                                                                                                                                                                                                      23-JUL-1993;
                                                                                                                                                                                             US5783665-A
                                                                                                                                                                                                               21-JUL-1998
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Best Local S
chimeric
                           Chimeric
                   Chimeric
                                                                                                                                                                                                                                                                                                      Baum PR,
                                                Key
Region
                                                                           Region
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The present sequence represents a fusion protien of the extracellular domain of a murine polypeptide, which a member of the cell development cycle protein family known as the Dellta family of mammanian membrane surface-bound ligands, and the human immunoglobulin G (IgG) Fc portion. The murine delta-related protein gene is expressed within vascular endothelium indicates a role for the polypeptides in the control of endothelial cell biology. The murine polynucleotide was identified from a white adipose tissue cDNA library. The polypeptide is useful for identifying receptors, which bind to and/or are activated by the polypeptide. The polynucleotide is useful in gene therapy of cerebral autosomal dominant ateriopathy with subcortial infarcts and leucoencephalopathy, an autosomal dominant disorder causing ischemic strokes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell development cycle protein of delta family useful for treating various disorders associated with central nervous system e.g. cerebral autosomal dominant ateriopathy and ischemic strokes
                                                                                                                                 346
                                                                                                                                                                                                                                                                347 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                  437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell development cycle; Delta family; membrane surface-bound ligand; endothelial cell biology; gene therapy; subcortial infarct; cerebral autosomal dominant ateriopathy; leucoencephalopathy;
                                                                                                                                                                 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
SHEDDFEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein of murine delta-related protein and human 1gG Fc.
                                                                                                                                                                                                                                                                                                   533..764 /note= "human IgG Fc portion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y68949 standard; Protein; 764 AA.
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- Homo sapiens.
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N-PSDB; V58006
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                                              14;
                                                                     shocekkvdrctsnpcangg------qclnrgpsrtcrcrpgftgthcelhisdca 446
                                                                                                                                    KHRSCPPGFGVVQAGT---PERNTVCKRCPDGF-----FSNETSSKAPCRKHTNCSV 147
                                                                                                                                                        FGLLLTQKGNATHDNICS------GNSESTQKCGIDVTVDKTHTCPPCPAPE 193
                                                                                                                                                                                                                                                     SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 373
                                              Gaps
                                                             -PCPDHYY 49
                                                                                            TDSWH-----TSDECLYCSPVCKELQYVKQECNRTHNRVCECKEG-----RYLEIEFCL 98
                                                                                                                                                                                                                      EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                      neurturin receptor alpha; NTNR-alpha; variant; chimeric; protein; immunoadhesion; ret-expressing cell; neurological;
                                                                                                                                                                                        LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                                                                                                                                                                                                                       Human neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
                                              88;
                              Length 764;
                                              Indels
                              DB 21;
                             ry Match 56.4%; Score 1283; DB 2:
t Local Similarity 59.8%; Pred. No. 4.1e-72
ches 271; Conservative 21; Mismatches 7:
                                                                                                                                                                                                                                                                                    KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
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fusion protein; immunoadhesion
renal; haematological disease.
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97US-0802805.
97US-0871913.
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18-FEB-1997;
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The present sequence represents human neurturin receptor alpha (NTNR-alpha)/FC sequence (IFF2a) fusion protein, from an example of the present invention. WINR-alpha proteins can be used: (a) to identify conclecules that bind specifically to it (potential agonists and indentify undecules that bind specifically to it (potential agonists and neutrurin (NTN); (c) to increase survival of Ret-expressing cells to neutrurin (NTN); (c) to increase survival of Ret-expressing cells or to activate Ret on the surface of cells (soluble glial derived neurotrophic factor receptor (GDNFR alpha) may be used the same way); (d) to increase the half-life of cognate ligands (especially NTN); (e) diagnostically to determine serum levels of its ligands; and (1) as confinal feed additive or molecular weight marker. NTNR-alpha, its genes, animal feed additive or molecular weight marker. NTNR-alpha, its genes, confinance and its ense nucleic acids, are useful in vivo drex vivo for treating conditions related to abnormal NTN activity or response, particularly neurological (central or enteric), renal or hematopoietic (spleen) diseases or injuries. Ab may be agonists or antagonists for therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-appression, e.g. in some tumours), also reagents for imminoassay and affinity purification.
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increasing survival of
e.g. neurological, renal and
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Pred. No. 1.3e-70;
25; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                   Example 3; Page 81-83; 116pp; English.
New polypeptide(s) based on human
related nucleic acid - useful for
ret-expressing cells for treating
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Best Local Simil
Matches 264; (
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14;

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664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; V58007.
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                     WO9836072-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1997;
09-JUN-1997;
                                                                                                                                                                                                 19-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-1998
                           406 G 406
                                                           663
                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                       - 6
                                                                                                                                                                    W71604;
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                                                           693
                                                                                                                    W71604
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                              οy
                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a neurturin receptor alpha (NTNR alpha) NTNR alpha binds neurturin. The NTNR alpha nucleic caid molecule is useful for the expression of NTNR alpha, which may be used to identify agonist and antagonist compounds having therapeutic applications, such
                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | || || || 324 --scrgsgnmeeece--kflr-dftenpclrnaiqafgngtdvnvspkgpsfgatgaprv 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 KQECNRTHNRVCECKEGRYLEIEF ...-CLKH ...----RSCP--PGFGVVQAGTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERNITVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 HCTAKWKTVCAPCP,DHY------YTDSWHTSDECLYCSPVCKELQYV 72
                                                         Human; neurturin receptor alpha; NTNR alpha; splenic haematopoiesis; anaemia; thrombocytopaenia; hypoplasia; haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agonist and antagonist compounds having therapeutic applications, su
as enhancing splenic haematopoiesis, treating anaemia,
thrombocytopaenia, hypoplasia, or haemorrhage. The present sequence
is a NTNR alpha and IgG (immunoglobulin G) fusion protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 ncrasyqtvts-cpadnyqaclgsyagmigfdmtpnyvdssptg---ivvspwc-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 IDVT------VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 telttniipgprdpvdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   acid sequence excluding the N-terminal signal peptide
                            Human NTNR alpha and 1gG fusion protein SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.3%; Score 1257.5; DB 21
62.7%; Pred. No. 1.3e-70;
ive 25; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Column 91-96; 78pp; English.
                                                                                                                                                                                                                                                                                                                          Klein RD;
                                                                                                                                                                                                                97US-0957063
                                                                                                                                                                                                                                            97US-0038839
97US-0049818
19-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                          Hynes MA, Rosenthal A,
                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-181808/16.
N-PSDB; 291459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention
                                                                                                         Homo sapiens
                                                                                                                                                                                                             24-OCT-1997;
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09-JUN-1997;
                                                                                                                                                    US6025157-A.
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Matches 264;
                                                                                                                       Synthetic.
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The present sequence represents rat neurturin receptor alpha

(NTNR-alpha)/Fc sequence (IFF2a) fusion protein, from an example of the

(NTNR-alpha)/Fc sequence (IFF2a) fusion protein, from an example of the

present invention. WTNR-alpha proteins can be used: (a) to identify

compounds that bind specifically to it (potential agonists and

antagonists) and to purify such compounds; (b) to modulate response of

calls to neutrurin (NTN); (c) to increase survival of Ret-expressing

cells or to activate Ret on the surface of cells (soluble glial derived

cells or to activate Ret on the surface of cells (soluble glial derived

controlly to determine serum levels of its ligands; and (f) as

can almal feed additive or molecular weight marker. WTNR-alpha, its genes,

contracting conditions related to abnormal NTN activity or response,

controllarly neurological (central or enteric), renal or haematopoietic

controllarly neurological (central or enteric), renal or haematopoietic

controllarly purification.

conditions antagonists to treat excessive/unwanted NTNR-

alpha expression, e.g. in some tumours), also reagents for immunoassay
                                      662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neurturin receptor alpha; NTNR-alpha; variant; chimeric; fusion protein; immunoadhesion; ret-expressing cell; neurological; renal; haematological disease.
Rat neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related nucleic acid - useful for increasing survival of ret-expressing cells for treating e.g. neurological, renal and haematological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide(s) based on human neurturin receptor alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 84-86; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenthal A;
                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                               W71604 standard; Protein; 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0957063.
97US-0802805.
97US-0871913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hynes MA, Klein RD,
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55.2%; Score 1254.5; DB 19; Length 664;

Best Local Similarity 62.8%; Pred. No. 2e-70; Matches 262; Conservative 30; Mismatches 56; Indels 69; Gaps 13;	as enhancing splenic haematopoiesis, treati thrombocytopenia, hypoplasia, on haemorrhe
32 HCTAKWKTVCAPCP-DHYYTDSWHTSDECLYCSPVCKELQYV 72 :	CC is a wink alpha and ige (immunoglobulin G) tusion protein from the CC present invention.  XX  SQ Sequence 664 AA;
73 KQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128	1; Length 664;
129 FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 179 : :::   :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : : :   : : :   : : :   : : : :   : : : : :   : : : : :   : : : : : :   : : : : :   : : : : : : :   : : : : : : : : : : : : : : : : : : : :	32 HCTAKWKTVCAPCP-DHYYTDSWHTSDECLYCSPVCKELQYV
180VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 229	274 ncrasyrtits-cpadnygaclgsyagmigidmtpnyvdsnptg1vvspwc 73 KQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF   :
230 DPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 289 	324 -ncrgsgnmeeecekilr-ditenpclrnaigafgngtdvnmspkg- 129 FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT : :::   :   :   :   :   :   :   :     :     :     :     :     :       :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :       :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :       :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :       :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :     :   :     :   :     :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :     :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
290 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 349 	ON 180VDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISKFDFUTCLVVVDVSHE 229  QY 180VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHE 229  ON 187 + Pisengardavak+ Phenomenal James of Fenbechelmistrander over 486
350 NYKTYPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406 	230 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALP
T 11 4 Y80124 standard; Protein; 664 AA.	Qy 290 APIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 349
Y80124;	QY 350 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLPG 406
19-MAY-2000 (first entry)	Db 607 nykttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnytqkslslspg 663
Rat NTNR alpha and IgG fusion protein SEQ ID NO:18.	
Human; neurturin receptor alpha; NTNR alpha; splenic haematopoiesis; anaemia; thrombocytopaenia; hypoplasia; haemorrhage.	KESULY 12 W70540 ID W70540 standard; Protein; 963 AA.
Rattus sp. Synthetic.	XX AC W70540; XX
US6025157-A.	26-JAN-1999 (fi
5-FBB-2000.	Integrin beta-1 chain.
24-OCT-1997; 97US-0957063.	
18-FEB-1997; 97US-0038839. 09-JUN-1997; 97US-0049818.	XX XX OS Homo sapiens.
(GETH ) GENENTECH INC.	Key
Hynes MA, Rosenthal A, Klein RD;	F.T. Peptide 120 /note= "signal peptide" FT Protein 21963
WPI; 2000-181808/16. N-PSDB; 291460.	
Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino acid sequence excluding the N-terminal signal peptide -	PN W09832771-A1. XX PD 30-JUL-1998.
Claim 3; Column 97-102; 78pp; English.	XX PF 29-JAN-1998; 98WO-JP00370.
The present invention describes a neurturin receptor alpha (NTNR alpha). NTNR alpha binds neurturin. The NTNR alpha nucleic acid molecule is useful for the expression of NTNR alpha, which may be used to identify	AA PR 29-AUG-1997; 97JP-0234544. PR 29-JAN-1997; 97JP-0015118. XX
nist and antagonist compounds having therapeutic applications, such	PA (TORAY IND INC.

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13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; beta-1 chain; immunoglobulin; chimeric; heterodimer complex; r; binding; ligand; blood platelet; hemostatic; diagnostic agent;
                                                                                                                                                                                                                                                                                                                                 ------VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                       546
                                                                                                                                                                                                                                                                                                                                                                                                      289
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                                                                                                                                                                                                                                                                                   EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 349
                                                                                                                                                       323
                                                                                                                                                                                          CNRTHNRVCECKEGRYLEIEF ---- CLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128
                                                                                                                                                                                                                            367
                                                                                       Gaps
                                                                                                                      -----YTDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslspg 663
                                                                                                                                                                                                              | ::|: : || |:|
asyrtits-cpadnyqaclgsyagmigfdmtpnyvdsnptg---ivvspwc-----
                                                                                                                                                                                                                                                                                                                                                                                                      VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                               ETSSKAPCRKHT-----NCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT
                                                   DB 21; Length 664;
                                                                                     69;
                                               55.2%; Score 1254.5; DB 21; Lengtl
62.8%; Pred. No. 2e-70;
ive 30; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..20
/note= "signal peptide"
21..963
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tandard; Protein; 963 AA.
                                                                                                                    AKWKTVCAPCP-DHY-----
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97JP-0015118.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         999 (first entry)
                                                                   Similarity 62.8
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-1 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TORAY IND INC.
664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-A1.
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RESULT 473513

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This represents an integrin beta-1 chain. The invention provides that integrin-immunoglobulin chimeric protein heterodimer complexes that comprise an integrin alpha or beta chain associated with an immunoglobulin light or heavy chain. These chimeric proteins form beterodimer complexes, in particular with a chimeric protein containing an integrin alpha chain and an immunoglobulin chain with a chimeric protein containing an integrin beta chain and an immunoglobulin chain; the immunoglobulin chain in each case may be a heavy chain, or one of the two may be a light chain. The integrin alpha chain is preferably beta is containing to a labba 2 and the integrin beta chain is preferably beta 1. Animal cells transformed with vectors containing the DNA coding for the above chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins can be used in the preparation of the chimeric proteins and their heterodimer complexes. The heterodimer complexes, which are useful for testing potential promoters and inhibitors of the binding of integrins to their ligands, function as blood platelet substitutes and
                                                                                                                                                Integrin-immunoglobulin chimeric protein heterodimer complexes as platelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the
                                                                                                                                                                                                                                                                           Claim 9; Pages 50-57; 87pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hemostatics and as diagnostic agents.
                                                                                                                                                                                                                              presence of plasma components
                            Tanaka T;
                                                                         WPI; 1998-427881/36.
                                                                                                   N-PSDB; V33773
                          Kainoh M,
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963 AA; Seguence

15; ----TNCSVFGLLLT 153 617 --vck-ctdpkfggqtcemcqtclgvcaehkecvqcrafnkgekkdtctgecsyfnitkv 673 674 esrdklpgpvgpdpvshckekdvddcwfyftysvngnnevmvhvvenpecptgpedpeep 733 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 297 -GFGVVQAGTPER 117 ------STOKCGI-----D 177 298 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 357 Gaps 34 TAKWKTVCAPCPDHY----YTDSWHTSDECLYCSPVCKELQYVKQ------EC 76 -----YLKQHC 33 VTVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 561 drsnglicggngvckcrvcecnpnytgsacdcsldtstceasnggicngrgicecg----Indels 130; Length 963; LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406 DB 19; 94; --RVCECKEGRYLEIEFC-LKHRSCPP------KCPPGT--55.1%; Score 1253; DB 19 51.6%; Pred. No. 3.9e-70; iive 32; Mismatches 94 NTVCKRCPDGFFSNETSSKAP-----CRKH-------1 ETFPPKYLHYDEETS--HQLLCD--Best Local Similarity 51.6 Matches 273; Conservative OKGNATHDNI - - - -Query Match 854 501 178 238 11 154 qq g g g g g ò g à ð ò ò δ ò qq õ ò

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This sequence is a fusion protein of the rabbit transforming growth factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The encoded protein is an example of a protein of the invention, which are isolated TGF-beta receptor fusion proteins that competitively inhibit binding of TGF-beta to TGF-beta receptor. The fusion protein can be used in a method for lowering the levels of TGF-beta in an individual having arthritis. It can also be used to treat medical conditions such as fibroproliferative disorders. The fibroproliferative disorder is a kidney, intraocular or pulmonary fibrosis, especially selected from alabetic nephropathy, of merulonephritis, proliferative collagen vascular disorders, including systemic sclerosis, to treat collagen vascular disorders, including systemic sclerosis, erythematosus. They can also be administered following coronary erythematosus. They can also be administered following coronary erythematosus. They can also be administered following coronary erythematosus.
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                                                                                                                                                 Transforming growth factor-beta receptor; TGF-beta receptor; arthritis; fusion protein; fibroproliferative disorder; diabetic nephropathy; glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disorder; therapy; rabbit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 KAPCRKHTNCSVFG---LLLTQKGNATHDNICSGNSESTQKCGIDVTVDKTHTCPPCPAP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 pkcimkek--kvfgetffmcscstdecndhiifseeyttsspdl---vdkthtcppcpap 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 wtriastipphyqksvnndmmytdnngavkfpqlckfcdvrsstcdnqkscmsncsit--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming growth factor-beta receptor fusion protein -
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18; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 1250.5; 65.2%; Pred. No. 2e-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koteliansky V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 18-19; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treat fibroproliferative disorders
 AA.
W73513 standard; Protein; 388
                                                                                                              Rabbit TGFbetaRII:Fc protein.
                                                                                                                                                                                                                                                                                                                                                          98WO-US07587.
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-609994/51
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Matches 257; Conserv
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                                                                                                                                                                                                                                                Oryctolagus sp.
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                                                                                                                                                                                                                                                                                                                                                              16-APR-1998;
                                                                        02-MAR-1999
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                                                                                                                                                                                                                                                                                                                                  Splice variant; rabbit; transforming growth factor-beta; TGF-beta; type II receptor; Fc portion; human IgG1; fusion protein; arthritis; fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis; diabetic nephropathy; glomerulonephritis; collagen vascular disease; polliferative vitreoretinopathy; myeLofibrosis; systemic sclerosis; polymyositis; scleroderma; dermatomyositis; systemic sclerosis; restenosis; wound; connective tissue production; adhesion; scarring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a splice variant of a rabbit transforming growth factor-beta (TGF-beta) type II receptor fused to the Fc portion of human IgG1. The fusion protein has higher affinity for TGF-beta than fusion proteins comprising the non-variant form of the receptor. The fusion protein contains soluble TGF-beta receptor constructs that are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TGF-beta. The protein competitively inhibits binding of TGF-beta to cellular receptors and/or forms an inactive complex with TGF-beta the protein is used to reduce levels of TGF-beta, for treatment of arthritic conditions associated with overexpression
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 252
                                                                                                PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 372
                                                                                                              Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.
            ellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpr
                                                            EEOYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of TGF-beta, especially fibroproliferative diseases, e.g. renal, intra-ocular or pulmonary fibrosis; diabetic nephropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion protein of a splice variant of transforming growth factor-beta receptor, for inhibiting the growth factor, e.g. in treatment of fibrosis
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                                                                                                                                                            DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                  Y54063 standard; Protein; 388
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                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       post-radiation fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                    27-MAR-2000
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collagen vascular disease, e.g. systemic sclerosis, polymyositis, scleroderma, dermatomyositis or systemic lupus erythematosus; and fibrosis associated with restenosis. It is also used for treating wounds, to prevent overproduction of connective tissue and so prevent adhesions or scarring, and to prevent post-radiation fibrosis (by administration to patients about to undergo radiation therapy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 KAPCRKHTNCSVFG---LLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKTHTCPPCPAP 192
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                      WKTVCAPCPDHYY----TDSWHTSDE-----CLYC---SPVCKELQYVKQECNRTHN 81
proliferative vitreoretinopathy; myelofibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                          17 wtriastipphyqksvnndmmytdnngavkfpqlckfcdvrsstcdnqkscmsncsit--
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                                                                                                                                                                                                                                                                                     Length 388;
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                                                                                                                                                                                                                                                                                   55.0%; Score 1250.5; DB 21; Lengt
65.2%; Pred. No. 2e-70;
ive 18; Mismatches 72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..358
/note= "human IL-R-alpha"
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359.360
'.nte= "Ala-Gly bridge"
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/note= "changed
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                                                                                                                                                                                                                                                                                                                                      257; Conservative
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                          388 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                            Sequence
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 VDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.0%; Score 1250; DB 20; Length 592; Best Local Similarity 84.0%; Pred. No. 3.4e-70; Matches 241; Conservative 10; Mismatches 28; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytokine antagonists - comprising extracellular domains of specificity-determining and signal-transducing components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                             Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 5; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                        (REGE-) REGENERON PHARM INC.
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93US-0140222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytokine receptor
Disulfide-bond
                                                                                                                                                                                                 27-NOV-1995;
                                                                                                                                                                                                                                                                   27-NOV-1995;
                                                                                                                                                                                                                                                                                                  20-0CT-1993;
                                                              US5844099-A
                                                                                                                                   01-DEC-1998
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Search completed: March 1, 2001, 09:17:06 Job time: 224 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2001, 09:20:09 ; Search time 135.68 Seconds

(without alignments)
348.998 Million cell updates/sec

Title: US-09-389-782A-7

Perfect score: 2264
Sequence: 1 ETFPPRYLHYDEETSHQLLC......VMHEALHNHYTQKSLSLSPG 404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
```

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% ... Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_15:*

1: \$P_archea:*
2: \$P_bacteria:*
3: \$P_tung!:*
4: \$P_tung!:*
5: \$P_tung!:*
6: \$P_tung!:*
7: \$P_mam.1:*
7: \$P_mhc:*
9: \$P_phage:*
10: \$P_phage:*
11: \$P_vagenet:*
12: \$P_vagenet:*
13: \$P_vagenet:*
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19: \$P_

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					SUMMAKIES	
		dР				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
п	1013	44.7	372	4	290нР4	O9uhp4 homo sapien
7	1013	44.7	401	4	000300	000300 homo sapien
3	892	39.4	401	1	008712	O08712 mus musculu
4	879	38.8	401	11	008727	008727 rattus norv
2	819.5	36.2	437	11	Q9R1A4	O9r1a4 mus musculu
9	433.5	19.1	300	4	095407	095407 homo sapien
7	406.5	18.0	302	13	OSPUS0	Ogous0 salvelinus
80	337.5	14.9	439	4	Q16042	016042 homo sapien
6	335	14.8	459	11	062327	062327 mus musculu
10	328	14.5	482	11	088734	088734 mus musculu
11	298	13.2	655	4	075509	
12	269.5	11.9	416	4	O9NPP6	Ognpp6 homo sapien
13	269.5	11.9	684	13	090544	090544 ginglymosto
14	268.5	11.9	384	4	Q9UP60	Ogup60 homo sapien
15	253.5	11.2	625	11	035305	O35305 mus musculu
16	252.5	11.2	616	4	09Y6Q6	09y6q6 homo sapien
17	239	10.6	349	12	057099	O57099 monkeypox v
18	237	10.5	349	12	057291	057291 monkeypox v
19	237	10.5	349	12	057100	O57100 monkeypox v

O57101 monkeypox v O57102 monkeypox v O57277 monkeypox v O57103 monkeypox v	057108 monkeypox v 057112 variola vir Q85407 variola vir	05710 camelpox vi 057110 variola vir 057111 variola vir				cowpox cowpox cowpox homo sap
057101 057102 057277 057103	057108 057112 Q85407	057098 057110 057111	Q89118 Q89098 O57116	057097 Q85308 057109 057305	057120 057122 073559 057118	057117 057113 057115 092956
1221	1222	1222	12 12 12	1222	2222	12224
349 349 348	348 348 348	3 3 4 4 9 4 4 9 9 9 9 9 9	349 349 350	349 349 449	326 326 351	351 350 347 283
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237 237 233.5 233.5	233.5 229 229 229	226.5 226.5 226 226	226 226 223	222.5 222.5 221 220.5	217.5 217.5 217.5 217.5	216.5 214.5 212.5 209.5
20 21 22 23	25 25 26	28 29 30	31 32 33	34 35 36 37	38 39 40 41	. 4 4 4 1 2 6 4 5

## ALIGNMENTS

0911HP4	1b4				
10.5	090нР4	PRELIMINARY;	PRT;	372 AA.	
ے ا	030AP4;	(Premarrel 13	Created		
DI		(TremBLrel. 13,	Last seq	sequence update)	
텀	01-OCT-2000	(TrEMBLrel. 15,	Last ann	annotation update)	
DΕ	OSTEOPROTEGE	OSTEOPROTEGERIN (FRAGMENT).			
SO	Homo sapiens (Human).	(Human).			
ပ္ပ	Eukaryota; Metazoa;	etazoa; Chordata;		Craniata; Vertebrata; Euteleostomi;	:omi;
ပ္ပ	Mammalia; Eu	Mammalia; Eutheria; Primates;			
×o	NCBI_TaxID=9606;	606;			
RN	[1]				
RP	SEQUENCE FROM N.A.	M N.A.		•	
22	TISSUE-PLACENTA;	NTA;			
Æ	He ZY., Ya	ZY., Yang GZ., Zhang	Zhang WJ., Wu XF.;	N XF.;	
RI	"Cloning and	Expression of C	Steoprot	and Expression of Osteoprotegerin from Homo sapiens	
R.	Sheng Wu Hua	Hsueh Yu Sheng Wu Wu Li Hsueh	Wu Wu Li	Hsueh Pac 31:680-684(1999)	. (6)
DR	EMBL; AF1341	87; AAF20168.1;			
8	HSSP; P25942	HSSP; P25942; 1CDF.			
DR	INTERPRO; IPR001368;	R001368;			
DR	PFAM; PF0002	PFAM; PF00020; TNFR_c6; 3.			
DR	PROSITE; PS0	PS00652; TNFR_NGFR_1;		WN_1.	
DR	٠.	PS50050; TNFR_NGFR_2;	2; 2.		
FI	NON_TER				
a	SEQUENCE 3	372 AA; 42758 MW;		F02527A5CD01CCD3 CRC64;	
Ġ				;	
7 Å	Query Matcn Best Local Similarity	44./%; larity 99.4%;	Score 1 Pred. N	Score 1013; DB 4; Length 372; Pred. No. 2.4e-81;	
W	Matches 174;	ū	0; Mismatches	1; Indels	0; Gaps
δy	1 ETFPPKY	LHYDEETSHOLLCDKC	PPGTYLKO	ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL	DECL 60
QQ	1 ETFPPKY	LHYDEETSHQLLCDKC	PPGTYLKQ	ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL	IIII DECL 60
δy	61 YCSPVCK	ELQYVKQECNRTHNRV	CECKEGRY	. YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCİKHRSCPPGFGVVQAGTPERNTV	RNTV 120
qq	 61 YCSPVCK		CECKEGRY		  RNTV 120
οy	121 CKRCPDG	FFSNETSSKAPCRKHT	NCSVFGLL	CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSG	175

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osteoprotegerin/osteoclastogenesis-inhibitory factor.";
Eur. J. Biochem. 254:685-691(1998).
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT. IN VITRO
OSTEOCLASTOGENESIS BY INTERPOTING CELL. 91-0-EBLL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROCENITYORS.
-!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).

-!- SUBCELLUIAR LOCATION: EXTRACELLUIAR.
-!- SUBCELLUIAR LOCATION: EXTRACELLUIAR.
-!- TISSUE SPECTIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
THE PARCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL, AB000146; BAA22910.1;
--- EMBL, AB000812; BAA32076.1;
--- EMBL, AB008812; BAA32076.1;
--- EMBL, AB008812; BAA32076.1;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97262071; PubMed=9108485; Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.; "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLRel. 15, Last annotation update)
OSTEOPROTECERIN PRECURSOR (SOTEOCLASTOGRNESIS INHIBITORY FACTOR)
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
121 CKRCPDGFFSNETSSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K., "Cloning and characterization of the gene encoding human
                                                                                                           Α
                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00652; TWFR NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TWFR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98151033; PubMed=9492069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98351569; PubMed=9688283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U94332; AAB53709.1; -. P25942; 1CDF.
                                                                                                                                                                                                                                                     INFRSF11B OR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00020; TNFR_c6; 3.
                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LUNG FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of bone density
                                                                                                                          060236
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                                                                                                  000300
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EMBL;
EMBL;
HSSP;
                                                               RESULT
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STRAINBALBAC: TISSUE-KIDNEY;
STRAINBALBAC: TISSUE-KIDNEY;
STRAINBALBAC: TISSUE-KIDNEY;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ETFPRYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CKRCPDGFFSNETSSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKSG 175
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
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EB42FA51C9D7C71E CRC64;
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Pred. No. 2.6e-81;
0; Mismatches 1
                                                OSTEOPROTEGERIN.
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POTENTIAL.
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Cytokine; Signal.
BY SIMILARITY
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                                                                                                                     TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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01-UUL-1997 (TrEMBLrel. 04, Created)
01-UL-1997 (TrEMBLrel. 04, Last seq
01-UL-2000 (TrEMBLrel. 15, Last and
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STRAIN-129/OLA, AND NIH SWISS;
MEDLINE-98382527; PubMed-9714833;
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99.48;
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401 AA;
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Glycoprotein;
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Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga Higashio K.;
Higashio K.;
"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
gene and its expression in embryogenesis.";
Gene 215:339-343(1998).
                                                                                                                                         15 TO DAY 17.

SINILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

Li. 1094331; AAB53708.1; -.

Li. AB013899; BAA28269.1; -.

Li. AB013899; BAA33388.1; -.

Li. AB013900; BAA33388.1; JOINED.

Li. AB013900; BAA33388.1; JOINED.

Li. AB013901; BAA33388.1; JOINED.

Li. AB013902; BAA33388.1; JOINED.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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PROSITE: PS00622; TNFR_NGFR_1; UNKNOWN_1.
PROSITE: PS50017; DEATH_DOMAIN; 1.
PROSITE: PS50050; TNFR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
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INTERPRO; IPR000488;
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EMBL;
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Cell 89:309-319(1997).
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCOMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
                                                                                                                                                                                                                                                                                                                                                                        Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                  Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto Derose M., Ellott R., Colombero A., Tan H.-L., Trall G., Sullivan Davy E., Bucay N., Renshaw-Geeg L., Hughes T.M., Hill D., Pattison Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: EXTRACELLULAR.
-:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL: U94330; AAB53707.1;
--- HSSP; P25942; LCDF.
             121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSG 175
                                                                                                                              01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTEOPROTEGERIN. 4 X TNFR-CYS.
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TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
POTENTIAL.
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1.
                                                                                                                 (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last seq
                                                                                          PRT;
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PFAM; PF00120; TURR_CG; 4.
PROSITE; PS0065; TURR_CGFR_1;
PROSITE; PS50050; TURR_NGFR_2;
                                                                                         PRELIMINARY;
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SIGNAL 1 21
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Pred. No. 1.2e-70;
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7; Mismatches

Matches 152; Conservative

Local Similarity

Query Match

39.4%; 86.9%;

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Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.; Gegenomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20122600; PubMed=10655513;
Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T., "Overexpression of M68/DGR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelepstomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TRG) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736(1999).
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                                                                       Last sequence update)
Last annotation update)
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EMBL; AF134240; AAD29688.1; -.
EMBL; AF217796; AAF35244.1; -.
EMBL; AF217794; AAF35685.1; -.
EMBL; AF217794; AAF35685.1; -.
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                     300
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PROSITE; PS01186; BGF_2; UNKNOWN_1.
PROSITE; PS50050; TNRR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
                095407 PRELIMINARY; PRT; 305407; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequil-oct-2000 (TrEMBLrel. 15, Last anno DECOY RECEPTOR 3 (M68) (M68C) (M68E).
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MEDLINE-99253915; Pubmed-10318773;
                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=990872321;
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INTERPRO; IPR001368; -.
PFAM; PF00020; TNFR_C6; 4.
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                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal
                                                                                                                                                                                                                           217 CKPCICIVPEV---SSVFIFPPRPKDVLITLTPRVTCVVVDISKDDFEVQFSWFVDDVE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 241
                                                                                                                         Gaps
                                                                                                                                                           ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                             81
                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
MUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
                                                                                                                                                                                                                                                                                                                 142 CKRCPDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNVCSGNREATQNCG 196
                                                                                                                                                                                                                                                                                               121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust mo antibody (Mab 7, its light and heavy chains) and construction single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL, GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; --
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 819.5; DB 11; Length 437; llarity 62.8%; Pred. No. 3.2e-64; Conservative 43; Mismatches 35; Indels 5;
                                                                                       Length 401;
                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                POTENTIAL.
FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                  Score 879; DB 11;
Pred. No. 1.7e-69;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     437
   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; ig; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                     M.
                                                                                     38.8%;
85.1%;
                                   46192
                                                                                     Query Match 38.8 Best Local Similarity 85.1 Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR003006; -.
   178
289
178
289
401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Best Local Simi
Matches 140;
   CARBOHYD
CARBOHYD
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65 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 124 153 64 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKSG 175 Length 300; DB 4; Pred. No. 2.1e-30;

> 362 394

d ò q ò g ð RESULT

us-09-389-782a-7.rspt

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VARIANT
VARIANT
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                                                                                                                                                                SEQUENCE FROM N.A.

Bobe J., Goetz F.W.;

A tumor necrosis factor receptor homolog is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";

Biol. Reprod. 0:0-0(1999).

EMBL; AF156738; AAD56428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 YVKQECNRTHNRVCECKEGRYL -- EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         | : ::||:|||||||: |:| |:| || || DRYSGLSIVCDRCPPGTYTERAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-MCAENQ 85
                                                                                                                                                                                                                                                                                                                                                                                                            11 DEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-91370690; PubMed=1966549;
Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
Brockhaus M., Lesslauer W.;
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
NCBL_TaxID=8038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences.";
Cytokine 2:231-237(1990).
EMBL; 563368; ABB19824.1; -.
HSSP; P25942; lCDF.
INTERPRO; IPR001368; -.
PFAM; PF00020; TNFR_C6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  Length 302;
                                                                                                                                                                                                                                                                                                                                                              18.0%; Score 406.5; DB 13; Length 43.1%; Pred. No. 5e-28; tive 32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 AA; 34037 MW; E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09, Last sequence update)
15, Last annotation update)
                                                                Last sequence update)
Last annotation update)
                             302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 AA.
                                                                                                                                                                                                                                                                     PFAM; PF00020; INFR_c6; 4.
PROSITE: PS00652; INFR_NGFR_1; UNKNOWN_1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
PROSITE: PS50050; INFR_NGFR_2; 1.
                                                     Created)
                                                                                   DECOY RECEPTOR.
Salvelinus fontinalis (Brook trout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                              PRT;
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01-JAN-1999 (TrEMBLrel. 09, Las
01-OCT-2000 (TrEMBLrel. 15, Las
TUMOR NECROSIS FACTOR RECEPTOR.
                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 43.1% hes 72; Conservative
                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                   HSSP; P19438; IEXT.
INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                     Receptor
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q16042;
                            Q9PUS0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---EVTCVVVDVSHEDP----EVKFNWYVDGVEVHNAK-TKPREEQYNSTYRVVSVLTV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK----- 318
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       69 LQYVKQECNRTHNRVCECKEGRYLEI ----- EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 IIGVVNCVIMTQVKKKPLCLQREAK----VPHLPADKARGTQGPEQQH------LLIT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 APSSSSSLESSASALDRRAP-----TRNOPQAPGVEASGAGEARASTGSSDSSPG 351
                                                                                                                                                                                                                                                         HYDEETSHOLLCDKCPPGTYLKOHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVSTRSQHTQPTPEPSTAPSTSFLLPMGPS----PPAEGSTGDFALPVGLIVGVTALGLL
                                                                                                                                                                                                                                                                                                                                                                                                                 123 RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                    89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                         Length 439;
                                                                                                                                                                                    Indels
                                                                    46090 MW; FEBCBE329CC67FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6C51D2CF1C4626DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NQVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 GHGTQVNVTCIVNVCSSSDHSSQCSSQASSIMGDIDSSPSESP 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
                                                                                                                                     ; Score 337.5; DB 4;
; Pred. No. 9.4e-22;
44; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NOD;
MEDLINE=95178848; PubMed=7873884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEAM; PF00020; TNFR_C6; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
       ω.
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PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
PRODOM; PD000771; -; 1.
                                                                                                                                       14.9%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48686 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mamm. Genome 5:726-727(1994)
                                                                                                                                     Query Match 14.9%
Best Local Similarity 26.6%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X76401; CAA53981.1;
HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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345
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                                                                  439 AA;
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268
345
421
459 AA;
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219 98 69 302

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CSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRA 163
                                                                                                   PERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSES---- 170
                                                                                                                                                                                                                                                                                                       --ESSASAGDRRAPPGGHPQARVMAEAQGSQE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOT-2000 (TrEMBLrel. 15, Last annotation update)
THER-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (THER-RELATED)DEATH
                                                                                                                                                                                                                                                                             KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPR
                                                                                                                    ---FLFPPKPKDTLMISRTPEVTCVVVD--VSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                     270 IGLIVGVTSLGLLMLGLVNCFILVQRKKRPSCLQRDAKVPHV-PDEKSQDAVGLEQQHLL
                                                                                                                                                                                          PRTLYVSQPEPTRSQPLDQEPG-----PSQTPSILTSLGSTP11EQSTKGGISLP
                                                                                                                                                                                                                                                                                                                                                     CSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGT
                                                                                                                                                             -----TQKSGGGGGGGGTCPPCPAPELL-------GGPSV-
                                                                                                                                                                                                                                                                                                                                      EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu
Vincenz C., Aggarwal B.B., Dixit V.M.;
"Identification and functional characterization of DR6, a n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parker A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF068868; AAC34583.1; -.
EMBL; AL096801; CAB75692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain-containing TNF receptor.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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PFAM: PF00531; death; 1.

PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE: PS50017; DEATH_DOMAIN; 1.

PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          655
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        TTAPSSSSSSL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR DJ181J13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P07174; 1NGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODOM; PD000771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                          12;
                                                                                                                                                  LQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGTPERNTVC 121
                                                                                                                                                                                                                                                                             QPEPTRSQPLDQEPG-----PSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGV 254
                                                                                                                                                                                                                                                                                                          ----FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 254
                                                                                                                                                                                                                                                                                                                                     ---ЕООН 304
                                                                                                                                                                                                                                                                                                                                                                  255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA---PIEKTISKAKGQPREPQVYTLPP 311
                                           Gaps
                                                                       9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                          YDRKA--QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCST 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
"The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure and Characterization of the two Transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                          KRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSES------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 106;
                                          96;
                                                                                                                                                                                                                                                   ---GGPSV---
            Length 459;
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                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            SSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 403
                                                                                                                                                                                                                                                                                                                                                                                                                           SRDELTKNQVSLTCLVKGFYPSDIAVEWESN-----GQPENNYKTTP 353
                                                                                                                                                                                                                                                                                                                                     255 TSLGLLMLGLVNCFILVQRKKKPSCLQRDA--KVPHVPDEKSQDAVGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51106 MW; F6C15046B48FF83C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
            Score 335; DB 11;
Pred. No. 1.6e-21;
; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 328; DB 11;
Pred. No. 7.2e-21;
48; Mismatches 160;
                                                                                                                                                                                                                                                  -----TQKSGGGGGGGTCPPCPAPELL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, Y14619; CAA74969.1; -. EMBL, Y14620; CAA74969.1; JOINED. EMBL, Y14621; CAA74969.1; JOINED. EMBL, Y14622; CAA74969.1; JOINED. EMBL, Y14623; CAA74969.1; JOINED. EMBL, Y14679; CAA74969.1; JOINED. EMBL, Y14679; CAA74969.1; JOINED.
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                                        51;
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PROSITE; PS00652; TNFR.NGFR.1;
PROSITE; PS50050; TNFR.NGFR.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%;
24.5%;
            14.8%;
24.6%;
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                                           Conservative
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Best Local Simi
Matches 102;
                                        Matches 100;
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                                                                                               50;
                                                         Length 655;
                                                                                               Indels
48939391C4852A33 CRC64;
                                                                                             132;
                                                     Query Match 13.2%; Score 298; DB 4;
Best Local Similarity 27.8%; Pred. No. 4.6e-18;
Matches 87; Conservative 44; Mismatches 132
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9 HYDEETSHQLLCDKCPPGTYLKQHCT-----AKWKTVCAPCPDHYYTDSWHTSDECLY 61

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SEQUENCE
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SIGNAL
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126
                                                    PWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCAR 173
                                                                        127 GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGGGGTCP- 185
                                                                                                                    ----PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED-----PEVKF 233
                                                                                                                                 -----LSVTWSESGQN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 ICSGNSESTQKSGGG------GGGGGGTC------PPCPAPELL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 VTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQDVTVPCPVP--- 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 PPGFGVVQAGTPERNTVCKRC-PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular analysis of
                                                                                                                                                                                268 SSIQEGTVPDNTSSARGKEDVNKT--LPNLQVVNHQ---QGPHHRHIL--KLLPSMEATG
                               KELQYVKQECNÄTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD
                                                                                                  ---GILPS
                                                                                                                                                               NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular anal human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL389978; CAB97534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 42; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                        MBLrel. 15, Last sequence update)
ABLrel. 15, Last annotation update)
HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 269.5; DB 4 Pred. No. 8.6e-16;
                                                                                       Created)
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
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410 FSTRSLINITAVEWKSGAKYTCTASHPPSQSTVKRVIRNQKVDCRQTDI----SVSLLKP 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PFEEIWTQQTATIVCEIV---YSDLENIKVFWQVNGVERKKGVETQNPEWSGSKKSTIVS 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSWHTSDECLYCS-----PVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 EEWQSGVE-YTCSAKQDQSSTPVVKRTRKARVEPTKPHLRL------------354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPPGFGVVQAGTPERNTVCKRCPDGFFSNETS---SKAPCRKHINCSVFGLLLTQKGNAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
EMBL: U18701; AA848195.1; --
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphil; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRDEL-TKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 HDNICSGNSESTQ-KSGGGGGGGGGTCPP-------CPAPELLGGPSVFLFPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95183140; PubMed-7877689;
Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney
Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                              SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPG
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2FF9D2071CDA6DFD CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1.6e-15; 53; Mismatches 162;
                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.9%; Score 269.5; Best Local Similarity 26.2%; Pred. No. 1.6 Matches 100; Conservative 53; Mismatches
                                                                                                                                                                                                                                                                         684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; ig; 6.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL ANTIGEN RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFSCSVMHEALHN---HYTQKS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75224 MW;
                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01;
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=SPLEEN;
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16;

RESULT 14

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"A homologue of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 KTISK------AKGQP----REPQVYTLP-------PSRDELT--KNQVS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSRCEPGKYLSSKCTPTSDSVCLPCGPDEYLDTWNEEDKCL-LHKVCDAGKALVAV-DPG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 NRTHNRVCECKEGRY -- LEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STDKCKPWTNCTLLGKLEAHQGTTESDVVCS--SSMTLRR------PPKEAQAYL- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ALTANLWNWVNDACSSLSGNKESSGDRCAGSHSATSSQQEVCEGILLMTREE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGGGGTCPPCPAPELLG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSTYRVVSVLTVLHQDWLN------GKEY----KCKVSNKA-------LPAPIE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC---KELQYVKQEC 76
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N-LINKED (GLORAC. ..) (POTENTIAL).
N-LINKED (GLORAC. ..) (POTENTIAL).
WHY FBC11872E99511DBE CRC64;
                                                                                                                             -:- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
-:- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN (POPENTIAL).
-:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; AF019046; AAB86810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 -PSLIVL------LLFISVVVVAAIIFGV------YYRKGGK------
        MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR ACTIVATOR OF NF-KAPPA-B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                Transmembrane; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 253.5; DB 11;
; Pred. No. 3.6e-14;
41; Mismatches 146;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                           PEAM; PF00020; TNFR_c6; 3.
PROSITE; PS00620; TNFR_NGFR_1; UNKNO PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
PRODOM; PD000771; -; 1.
                                                                                                and dendritic-cell function."; Nature 390:175-179(1997).
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INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
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235
625
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153
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87
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155
176
106
175
625 AA;
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Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                 HSSP; P25942; 1CDF
                                                                                                                                                                                                                                                                                                                                                 Receptor;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GGG-----PPCPAPELLGGPSVFLFPPKP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 SGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPST-PPTP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-----DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 PERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 PDGNVVIACLVQGFFPQEP------LSVIWSESGQGVTARNFPPSQDA 90
                                                                                                                                                                                                                                                                                  down-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
RECEPTOR ACTIVATOR OF WE-KAPPA-B PRECURSOR (INF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73;
                                                                                                                                                                                                                                                                                  is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 384;
                                                                                                                                                                                                                                                                                a gene which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                           Zheng S., Cao J., Cao W., Cai X., Geng L.;
"Identification and characterization of SNC73, a gene wh
regulated in colorectal cancer.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF067420; AAC19365.1;
HSSP; P01825; 7FAB
                                                                                                                                                                                                                                                                                                                                                            INTERPRO, IPRO03006; -.
PFAM, PRO047; 19; 3.
PROSITE; PS0047; 19; 4.
SEQUENCE 384 AA; 40947 MW, BA7ADC3CA5A9DD48 CRC64;
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 268.5; DB 4;
Pred. No. 9.6e-16;
); Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 YSKLIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā.
                                                384
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                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.9%;
26.2%;
                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFRSF11A OR RANK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                               SNC73 PROTEIN.
                                                               09ub60;
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                                              09up60
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251

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δ

18;

Gaps

Indels 117;

Length 625;

δλ

294 KMVPEDGAGVCGPVCAAGGPWAEVRDSRTFTLVSEVETQGDLSRKIPTEDEYTDRPSQPS 353

QQ

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Search completed: March 1, 2001, 09:20:11 Job time: 409 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 1, 2001, 09:17:47 ; Search time 40.97 Seconds
(without alignments)
318.448 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-389-782A-7 2264 1 ETFPPKYLHYDEBTSHQLLC......VMHEALHNHYTQKSLSLSPG 404

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

88757 seqs, 32294092 residues Searched:

88757 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	рошо	homod	homo sapien	homo sapien	oryctolagus	cavia porce	mus musculu	rattus norv	mus musculu	rattus norv	mus musculu	mus musculu	rattus norv	mus musculu	mus musculu	mus musculu	rattus norv	mus musculu	mus musculu	homo sapien	mus musculu	rattus norv	homo sapien	mns	mus musculu	рошо	homo	oryct	oryctolagus	mesocricetu		3	canis famil
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	De	P0	P0	PO	P0	P0	PO	P2	P2	P0	P2	PO	PO	P2	P0	P0	PO	P2	P0	P0	PO	P0	P0	P0	DQ	P0	PO	P2	P0	PO	P0	P2	P2	Ь0
SUMMARIES	ID	GC1_HUMAN	GC2_HUMAN	GC4_HUMAN	GC3_HUMAN	GC_RABIT	GC2_CAVPO	GC3_MOUSE	GCB_RAT	GC3M_MOUSE	GC1_RAT	GC1_MOUSE	GC1M_MOUSE	GCC_RAT	GCAA_MOUSE	GCAM_MOUSE	GCAB_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	MUCB_HUMAN	EPC_MOUSE	EPC_RAT	MUC_HUMAN	MUC_MOUSE	MUCM_MOUSE	EPC_HUMAN	TNR2_HUMAN	MUC_RABIT	MUCM_RABIT	MUC_MESAU	MUC_SUNMU	TNR2_MOUSE	MUC_CANFA
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	Length		326	327	290	323	329	329	333	398	326	324	393	329	330	399	335	322	336	405	391	421	429	454	455	476	428	461	458	419	454	457	474	450
ф	Query Match	m	50.2	20.0	49.7	40.2	39.3	37.2	37.1	36.9	36.4	35.9	35.9	35.5	35.5	35.5	35.2	34.5	34.2	34.2	15.9	15.6	15.6	15.6	15.6	15.3	15.2	15.0	14.9	7	•	14.6	14.6	14.6
	Score	1204	1137.5	1133	1125.5	606	890.5	841.5	840	835.5	824.5	812.5	812.5	804.5	804	804	797	780.5	774	774	360.5	353.5	353	353	352.5	347.5	343	339.5	337	332	331.5	330.5	330.5	329.5
	Result No.	1	7	m	4	ហ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P23085 heterodontu	P23087 heterodontu	P01879 oryctolagus	P23088 heterodontu	P23086 heterodontu	P27512 mus musculu	P01875 gallus gall	P23084 heterodontu	P01877 homo sapien	P01876 homo sapien	P20758 gorilla gor	P25942 homo sapien
HVC2_HETFR	HVCS_HETFR	ALC_RABIT	HVCM_HETFR	HVC3_HETFR	CD40 MOUSE	MUC_CHICK	HVC1_HETFR	ALC2_HUMAN	ALC1_HUMAN	ALC1_GORGO	CD40_HUMAN
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438	438	299	461	393	289	446	370	340	353	353	277
13.4	13.2	13.0	13.0	12.7	12.5	12.5	12.3	11.9	11.9	11.8	11.7
304.5	298	295	294	287	284	282.5	277.5	269.5	268.5	267	264
34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

ALIGNMENTS	ULT 1 _HDMAN GOL-HUMAN STANDARD; PRT; 330 AA.	FULBS), 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update)	(Rel. 38, Last	IG GAMMA'I CHAIN C KEGION. IGHGI.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		SEQUENCE FROM N.A. MEDLINE-82274238; PubMed=6287432;	Ellison J.W., Berson B.J., Hood L.E.;	c gammar gene.	[2]	SEQUENCE OF I-135 (MYELOMA PROTEIN EU). MEDLINE=71064024: PubMed=5489771:	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,		The covarent structure of a numban gamma G-immunogrobulin, vii. Amino acid sequence of heavy-chain cvanoden bromide fragments H1-H4."	lemistry 9:3161-3170(1970).	[3] CEOTIENCE OF 126-220 (FIT)	MEDLINE=71064025; PubMed=5530842;	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,	Edelman G.M.;	a muman gamma s-immunogiopuiin. s: in cvanogen bromide fragments H5-H7.	nemistry 9:3171-3181(1970).		SEQUENCE (MYELUMA PROTEIN NIE). MEDIINE=77070269: DubMed=826475:		"The rule of antibody structure. The primary structure of a	monocional 1961 immunoglobulin (myeloma procein Nie). 111. Ine chymotryptic peptides of the H-chain, alianment of the tryptic	peptides and discussion of the complete structure.";	Hoppe-Seyler's 2. Physiol. Chem. 357:1571-1604(1976).	[3] SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.	MEDLINE=83289131; PubMed=6884994;	Hilschmann N.;	"inree-dimensional structure determination of antibodies. Frimary structure of crystallized monoclonal immunoglobulin IdG1 KOL, I.":	•	[6]	DISULFIDE BONDS.	meDLINE-/100402/; rubmed-4923144; Gall W.E., Edelman G.M.;	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";	
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                                                                                              "Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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K -> R (IN GLM(3) MARKER).
FTIG-VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FTIG-VAR_003887.
/FTIG-VAR_003887.
/FTIG-VAR_003888.
REMOVED POST-TRANSLATIONALLY.
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                              Dreker L., Schwarz J., Reichel W., Hilschmann N.;
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                                                                                  X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; Pubmed=7236608;
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                      MEDLINE=77070267; PubMed=1002129;
Biochemistry 9:3188-3196(1970).
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PDB; 1FC2; 15-JUL-92.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         3770EE106C2FA33D CRC64;
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                                                                                             53.2%; Score 1204; DB 1;
100.0%; Pred. No. 6.3e-74;
ive 0; Mismatches 0;
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Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                       SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human igG2 myeloma protein.";
Can. J. Blochem. 57:758-767(1979).
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REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
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"A note of the amino acid sequence of immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
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CH2.
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MEDLINE-80114419; PubMed-118920;
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PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immun
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                                                                                                                                                                                                                                                                                     184 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 243
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SEQUENCE OF 1-30 AND 81-326.

MEDLINE-7020560; PubMed-4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Pluk J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Pluman immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                        AT OR NEAR THE COMPLEMENT-BINDING SITE. REMOVED POST-TRANSLATIONALLY (PROBABLE).
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo:
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Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
                                                                                                                                                                                                                               ;
                                                                                                                                                            Score 1137.5; DB 1; Length 326; Pred. No. 1.7e-69; 8; Mismatches 4; Indels 1;
                                                                                 8310878C6878CF9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
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PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-4 CHAIN C REGION.
/FTId=VAR_003889
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CH2.
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                                                                                    35884 MW;
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94.1%;
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Best Local Similarity 94.1'
Matches 208; Conservative
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INTERPRO; IPR003006; -
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG MHC
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                                                                                                                                                                                             GGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
                                                                                                                                                                                                                           PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-81021548; PubMed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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MEDLINE-82247835; PubMed-6808505;
MACAINGER A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy Chain disease in man: cDNA sequence supports partial gene deletion model.";
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 12-97 OF PROTEIN WIS.
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=77021516; PubMed=823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.; The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
CH3.
INTERCHAIN (WITH A LIGHT CHAIN).
                             CHAIN).
                                                                                                   Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
                                                                                                                         8; Indels
                                                                      35940 MW; 3EDBD811EF208E7A CRC64;
                             (WITH A HEAVY (WITH A HEAVY
                                                                                                                                                                                                                                                                  404
                                                                                                                                                                                                                                                                             283 SFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLG 326
                                                                                                                                                                                                                                                                  SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                   Score 1133; DB 1;
Pred. No. 3.5e-69;
8; Mismatches 8;
                             INTERCHAIN
                                                                                                   50.0%;
92.9%;
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
327
14
83
106
109
201
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                                                                        AA;
                                                                                                              Similarity
                                                                                                               Best Local Sin
Matches 208;
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P01860;
                                       DISULFID
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                                                                                                                          DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
                                                                                                                                                 AND ALL OF THE CH1 REGION.

**MISCELLANDORS: DISBASE PROFEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.
                                                                                                                                                                                                                                             MISCELLANDONS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCIASS.

MISCELLANDONS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OFFER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                   MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN. MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN PROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...) CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; Immunoglobulin C region; Glycoprotein.
73 HINGE.
1 183 CH2.
289 CH3.
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E69CBC95705B2F46 CRC64;
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/FIId=VAR_003890.

P -> L (IN OMM).

/FIId=VAR_003891.

F -> Y (IN OMM).

/FIId=VAR_003892.
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S -> N (IN OMM).
/FTId=VAR_003894.
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/FTId=VAR_003895
F -> Y (IN OMM).
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INTERPRO; IPRO00495; -...
INTERPRO; IPRO03006; -...
FRAM; PFO0047; ig; 2...
PROSITE; PSO0290; IG_MHC; 1...
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                                                                                                   REF.2.
MISCELLANEOUS:
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Length 290;

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DB

49.7%; Score 1125.5;

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GC2_CAVPO
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"Nucleotide sequence of a rabbit 1gG heavy chain from the recombinant
                                                                       153 TQKGNATHDNICSGNSESTQKSGGGGGGGGTCPPCPAPELLGGPSVFLFPPKPKDTLMIS 212
                                                                                                                  272
                                                                                                                            SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 392
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                               97 CLKHRSC---PPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAP-CRKHTNCSVFGLLL 152
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                                                                                                                                                          NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                   27 CPEPKSCDTPPP-------CPRCPEP-KSCDTPPPCPRCPEPKSCDT----
                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-8329911; PubMed-6193512; Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; Heavy chain genes of rabbit 196: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the Fd sections of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-70110015; PubMed-5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of
 Pred. No. 9.8e-69;
9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA CHAIN C REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence studies on the constant region of immunoglobulin G of different allotype."; 31ochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-84030930; PubMed-6313520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=76135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 129-131 AND 155-322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emmunogenetics 18:387-397(1983)
           19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 88-266 FROM N.A.
69.68;
          Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                           393 HYTQKSLSLSPG 404
                                                                                                                                                                                                                                                              278 RFTQKSLSLSPG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 132-161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE OF 1-128.
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haplotype
             217;
                                                                                                                                                                                                                                                                                                                  GC_RABIT
P01870;
          Matches
                                                                                                                                                                              158
                                                                                                                 213
                                                                                                                                    86
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                                                                                                                                                                                                                                                                                              RESULT
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P01862;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last cannotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 GAWMA-2 CHAIN C REGION.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 -> M (IN D11 MARKER).
1 -> A (IN B15 MARKER).
1 -> E (IN REF. 2).
2 -> E (IN REF. 3 AND 4).
2 -> E (IN REF. 3 AND 5).
3 -> E (IN REF. 5).
3 -> E (IN REF. 5).
4 -> D (IN REF. 5).
5 -> E (IN REF. 5).
5 -> E (IN REF. 5).
6 -> E (IN REF. 5).
7 -> E (IN REF. 5).
8 -> D (IN REF. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 909; DB 1;
Pred. No. 3.3e-54;
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30; IG_MHC; 1.
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ilarity 72.8%;
Conservative 28
                                                                                                                                                                                                                                                                                                                                                       EMBL; M16426; AAA31289.1; -.
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INTERPRO; IPR003006; -.
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280
284
323
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PFAM; PF00047
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Best Local Si
Matches 163
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MEDLINE-71058474; DibMed-4922544;
Ollveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Blochemistry 10:26-31(1971).
-1- MISCELLANDUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN PIR; A02151; G2GP.
                                                                                                                                               pig
the carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| : | : | : | : | | | GLYSLTSMYTVPSSQKATCNVAHPASSTKVDKTVEPIRTPZPBPC------TCPK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 246
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                                               Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                   Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                     SEQUENCE OF 227-311.
MEDLINE-7036079.
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain; Immunoglobulin C region; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                   Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 890.5; DB 1
Pred. No. 5.8e-53;
}; Mismatches 64
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         to the PIR data bank
                                                                                                                                                                                               SEQUENCE OF 134-226.
MEDLINE=75036072; PubMed=4429665;
                                                                                                               SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                         MEDLINE=71058471; PubMed=5538606;
                                                                                                                                                                                                                                        antibodies.";
Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                         Biochemistry 13:4804-4811(1974).
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60.7%; Pre
tive 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
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107
110
202
178
Trischmann T.M.;
Submitted (APR-1975)
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142
178
248
329 AA;
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                              SEQUENCE OF 4-68
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Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation.

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  364
                    301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
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  YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine 1963 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.2%; Score 841.5; DB 1; Length 329; 66.5%; Pred. No. 1.1e-49; ive 35; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F45827174182BAD6 CRC64;
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                                                                                       365 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                         GC3_MOUSE STANDARD; PRT; 329 AA. P22436; 01-A0G-1991 (Rel. 19, Created) 01-A0G-1991 (Rel. 19, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
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HINGE.
CH2.
CH3.
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PROSITE; PS00290; IG_MHC;
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INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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223
327
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224
329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 149;
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GC3_MOUSE
307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AQTPQVYIIPPPREQMSKKKVSLTCLVTNFFSEALSVEWERNGELEQDYKNTPPILLDSDG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 EVHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGR
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          MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine 19G3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                       The structure of the mouse immunoglobulin in gamma 3 membrane
                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.

NON TER 1 1 7 CH1.

DOMAIN 197 HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 398;
                                                                                              SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 TYFLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHTQKNLSRSP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.9%; Score 835.5; DB 1; ilarity 66.4%; Pred. No. 3.4e-49; Conservative 35; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH2.
CH3.
POTENTIAL.
                                                                                                                                                                                     Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                                EMBL; J00451; AAB59655.1; -. EMBL; V01526; CAA24767.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00047; 19; 3.
PROSITE; PS00290; IG_MHC; 1.
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INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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388
398 AA;
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P20759;
01-FEB-1991 (
01-FEB-1991 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 148;
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1444
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                                                                                                                                                                                                           Brueggemann M.;
Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
PIR, 1473-482(1988).
PIR, PS0018, PS0018.
INTERPRO; IPR000495;
INTERPRO; IPR00047;
INTERPRO; IPR00047;
INTERPRO; IPR00047;
ISPROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 SNETSSKAPCRKHTNCSVFGLLLFQKGNATHDNICSGNSESTQKSGGGGGGG----GTCP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 SSVTSSTWPSQTVT-C------NAHPASSTKVDKKVERRNGGIGHKCPTCPTCH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 305
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                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthería; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                       HEAVY CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.1%; Score 840; DB 1; Length 333; 57.0%; Pred. No. 1.4e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36497 MW; 55F8B64D48D460A6 CRC64;
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INTERCHAIN (WITH A H
INTERCHAIN (WITH A H
INTERCHAIN (WITH A H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                  domain; Immunoglobulin C region.
                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2B CHAIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AA.
                                        333 AA.
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                                         PRT;
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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P03987;
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                                      GCB_RAT
P20761;
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ID GC3M_MC
DT 23-0CT
DT 13-0CT
DT 15-JUL
DE IG GAM
OS MUS mU
OC EUKATY
OC MARMATI
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           RESULT
GCB_RAT
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184 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 241
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324 AA;
                                                                                                                                                                                                                                                                                                                                                    PIR; A02159; G1MS
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27
102
104
107
                                                                                                                                                               murine myeloma
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                                                                                                                                              Adetugbo K.;
                                                                                                    heavy chain.
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CONFLICT
SEQUENCE
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                                                         Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                    KGQPREPQVYILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 357
                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                          181 GGTCPPCPAPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 237
                                                                                                                                                                                                                                                                                                                                           DGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 297
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

BEDLINE-80045036; PubMed-115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Gloning and complete; nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL) 013BAB45EF49B9DA CRC64;
                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                CHAIN).
                                                                                                                                                                                                                                                                         Length 326;
                                                                                                                           Immunoglobulin C region; Glycoprotein
                                                                                                                                                                                                       CHAIN)
CHAIN)
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                      HEAVY
HEAVY
HEAVY
HEAVY
                                                                                                                                                                                                                                                                         Score 824.5; DB 1;
Pred. No. 1.5e-48;
41; Mismatches 36;
                                                                                                                                                                                      (WITH A H                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 AA
                                                                                                                                                                                             INTERCHAIN (INTERCHAIN (INTERCHAIN (
                                                                                                                                                                                       INTERCHAIN
                                        SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed-3149946;
                                                                                                                                                                                                                                                 MM;
                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                         36.4%;
                                                                                        INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
GAMMA-1 CHAIN C REGION.
                                                                                                                                                                                                                                                 35946
                                                                                                                                                                                                                                                                                          Conservative
        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                         Immunogiobulin domain;
NON_TER 1 1 97
                                                                         Gene 74:473-482(1988).
PIR; PS0017; PS0017.
                                                                                                                                                                                                                                                 326 AA;
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                         Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GC1_MOUSE
P01868;
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DISULFID
DISULFID
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                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDILINE=80012837; PubMed=113776;
RSOgers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                           Shimizu A.,
SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=73008889; PubMed=5073237;
Svasti J, Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evolution of immunoglobulin subclasses. Primary structure
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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62.3%; Pred. No. 9.4e-48;
live 44; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 6:3305-3321(1979).
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HINGE.
CH2.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (MYELOMA PROTEIN MOPC 21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rine myeloma gammal chain.";
Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=78242288; PubMed=98524;
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PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 62.3%
Matches 139; Conservative
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INTERPRO; IPR000495; -.
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
"Nucleotide sequences of gene segments encoding membrane domains of
proc. Natl. Acad. Sci. U. S.A. 79:2623-2627(1982).
-I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MENA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANY SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND LAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCOBED
IN SEBARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
                                                                                                                                         302 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-80045036; PubMed=115593; Monjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y., "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                            242 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MEDILINE-82115295; PubMed-6799207;
ROGERS J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Elsenberg D., Wall R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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01-NG-1991 (Rel. 19, Last sequence update)
01-NMY-2000 (Rel. 39, Last annotation update)
IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
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Cell 18:559-568(1979).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Brueggemann en rat inmunoglobulin gamma 2c heavy chain constant
region CDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
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CYTOPLASMIC (POTENTIAL).
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2C CHAIN C REGION.
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                                     PIR; B02159; GIMSM.
MGD; MGI:96446; IGH-4.
INTERPRO; IPR000495; -
INTERPRO; IPR003006; -.
PFAM; PF00047; 19; 3.
PROSITE; PS00290; IG_MHC; 1.
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V00793; CAA24172.1;
V00793; CAA24173.1;
V00793; CAA24174.1;
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Matches 139; Conservative
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Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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     Usage
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31-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-2A CHAIN C REGION, A ALELE.
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llarity 63.7%;
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 3.
PROSITE; PS00290; IG_MHC; 1.
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Eukaryota; Metazoa;
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Matches 142;
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                                                                                                                                                                                                                   Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse 1gG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
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Julo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain gen
suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma G2
immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Blochem. 30:452-462(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMOVED POST-TRANSLATIONALLY.
B84361C5445A6864 CRC64;
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                                                                                                                      Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%; Score 804; DB 1;
65.0%; Pred. No. 3.5e-47;
iive 30; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin C region.
                                                                                                                                                                                             MEDLINE=74175517; PubMed=4831970;
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PROSITE; PS00290; IG_MHC; 1.
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                                                                                                  family.";
Proc. Natl. Acad.
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NON_TER
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
4C38138BFAED3FF0 CRC64;
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INTERCHAIN (WITH A HEAVY CHAIN).
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65.0%; Pred. No. 4.4e-47;
tive 30; Mismatches 46; Indels
                      21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
399 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00471; AAB59661.1; ALT_INIT.
                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=82222190; PubMed=6283537;
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PROSITE; PS00290; IG_MHC; 1.
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STANDARD;
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INTERPRO; IPR000495; -.
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399 AA;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

; Search time 79.26 Seconds March 1, 2001, 09:15:48 Run on:

(without alignments)
346.100 Million cell updates/sec

US-09-389-782A-7 Title:

1 ETFPPKYLHYDEETSHQLLC.......VMHEALHNHYTQKSLSLSPG 404 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 Total number of hits satisfying chosen parameters:

195891 seqs, 67900655 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR_66:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Iq qamma-1 chain C						gamma-3		gamma-4	gamma-	gamma		gamma	gamma 4	gamma-2	gamma 1	gamma		gamma-	Ig heavy chain C r	Ig gamma-1 chain -	Ig gamma-2b chain	датта-3	Ig gamma-1 chain C	~	Ig gamma-1 chain C	Ig gamma-1 chain C	gamma-2c	Ig gamma-2a chain
ID	531866	Снни	S72664	869339	PT0207	A23511	A60764	GZHU	G4HU	G3HUWI	GHRB	147160	147159	147162	G2GP	147158	147161	S22080	G3MSC ·	C30554	S31459	PS0018	G3MSM	PS0017	PC4436	G1MS	G1MSM	S00847	G2MSA
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% Query Match Length	53.2	53.2	53.1	52.9	51.3	50.6	50.6	50.2	20.0	49.7	40.2	39.9	39.9	39.8	39.3	38.9	38.6	37.6	37.2	37.1	37.1	37.1	Φ	36.4	36.3	35.9	35.9	35.5	35.5
Score	1204	1204	1202	1198	1162	1146.5	1144.5	1137.5	1133	1125.5	606	902.5	902.5	900.5	890.5	880.5	874.5	850.5	841.5	841	841	840	835.5	824.5	822.5	812.5	812.5	804.5	804
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	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C; Species: synthetic
A; Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C; Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C; Accession: S31866
R; Filpula, D.
submitted to the EMBL Data Library, February 1993
A; Pescription: Screeing method for protein-protein interactions of cloned gene produc
A; Reference number: S31866
A; Accession: S31866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C, Reywords: 1mmungalobulin
F:1-22/Region: Bscherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
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                             gamma-1 chain C region - synthetic
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A; Residues: 1-255 <FIL>
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RESULT

Ig gamma-1 chain C region - human C; Species: Homo sapiens (man) C; Species: Homo sapiens S38861; S33887; B90563; A90564; B91668; A91723; A02146 R; Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A; Reference number: A93433; MUID:82274238

; 0

Gaps

; 0

362

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C; Complex: An immunoglobulin heterotetramer subunit consists or two incurred than disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into c; superfamily: immunoglobulin c region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20-85/Domain: immunoglobulin homology <IM1>
F; 21-26f/Domain: immunoglobulin homology <IM2>
F; 243-310/Domain: immunoglobulin homology <IM3>
F; 27-83,144-204,250-308/Disulfide bonds: #status experimental
F; 103/Disulfide bonds: interchain (to light chain) #status experimental
F; 109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Journal Deavy chain V region precursor - human C; Species: Homo sapiens (man).
C; Species: Homo sapiens (man).
C; Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-N-C; Accession: S72664
R; Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A; Reference number: S72664
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-374 < KRNA
A; Residues: 1-374 < KRNA
A; Residues: 1-374 < KRNA
A; Residues: I-374 < KRNA
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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llarity 90.8%; Pred. No. 6e-68;
Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                          53.2%; Score 1204; DB 1;
100.0%; Pred. No. 4e-68;
ive 0; Mismatches 0
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A; Reference number: A91667; MUID: 77070267
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R;Cunningham, B.A.; Rutlashauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochamistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
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A; Molecule type: protein
A; Residues: 1-96, 7K. /98 - 135 < CUN>
A; Note: this sequence has the Glm(3) marker, 97-Arg
R; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
B; Rutishauser, J.; 1311. 1970
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A; Residues: 1.34, 0',36-96, K',98-115,0',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A; Residues: 1.34,0',36-96, K',98-115,'O',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A; Note: this sequence has the Glm(17) and Glm(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
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A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOH
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A; Molecule type: protein
A; Residues: 136.154, Q',156.165, Q',167.176, Q',178.194, N',196.197, D',199.238, E',240, A; Residues: 136.154, Q',156.165, Q',167.176, Q',178.194, N',196.197, D',199.238, E',240, A; Nonstingl, H.; Hilschmann, N.
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                                                                                                             Glm(1) markers,
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A; Molecule type: protein
A; Residues: 1-96, "R', 98-197, "D', 199-238, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
K; Gall, W. E.; Edelman, G. M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu
A; Reference number: A90565; MUID:71064027
A; Contents: annotation; disulfide bonds
                                                                       A;Cross-references: EMBL:217370
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the
A;Note: Lys-330 is removed after translation
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A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
                                                                                                                                                                                                            Library, October 1992
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R;Takahashi, w.; Ueda, S.; Obata, M.; Nikaido,
Cell 29, G71-679, 1982
A;Title: Structure of human immunoglobulin gamm
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A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1: 114/1; 224/1
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A;Contents: myeloma protein Nie
A;Accession: B91668
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Contents: myeloma protein Eu
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A;Residues: 88-113;235-330 <TAK>
                                                                                                                                                                             R; Harris, L.J.
submitted to the EMBL Data
A; Reference number: S33904
A; Accession: S36861
                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 2-330 <HAR>
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17-Mar-2000

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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
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A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
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                                                                                                                                                                                                                                                     Ig gamma-3 chain C region (allotype G3m(b)) - human
C.Species: Homo sapiens (man)
C.Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
  122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGG 180
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A, Map Position: 14q32.33-14q32.33
A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamilly: Immunoglobulin C region; Immunoglobulin
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66.0%; Pred. No. 1.7e-64;
tive 19; Mismatches 33;
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                                                                                                    199 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNYTQKS 234
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F; 20-85/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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Best Local S
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                                                                                                                                      C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C; Cacession: $69339
R; Khanlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: $69339; MUID:95262687
A; Accession: $69339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molcule type: mRNA
A;Rosidues: 1-774 <KHA>
A;Coss-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin.homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%; Score 1162; DB 2; ilarity 99.1%; Pred. No. 1.1e-65; Conservative 1; Mismatches 1;
                                                                                                                           Ig heavy chain V region precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 99.13
0; Conservative
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Best Local Similarity
365 OKSLSLSPG 373
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Matches 220;
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Whap position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds: In some cases, such as 1gA and 1gM, the subunits associate into Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin c region; immunoglobulin homology xIM2> F;20-85/Domain: immunoglobulin homology xIM2> F;313-202/Domain: immunoglobulin homology xIM3> F;34-500-00main: immunoglobulin homology xIM3> F;34-500-00main: immunoglobulin homology xIM3> F;34-500-00main: immunoglobulin homology xIM3> F;37-83,140-200,246-304/Disulfide bonds: #status experimental F;202,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                    and 264-268
60-Ala and in the
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Rilstein, C.; Frangione, B.
Builstein, C.; Frangione, B.
Buchem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A9023; MUID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Contents: annotation; Sa, disulfide bonds
C;Genetics: annotation; Sa, disulfide bonds
A;Concents: GDB:I19338; OMIM:147110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a human immunoglobulin C-gamma4 MUID:83157104
                                                           A; Molecule type: protein
A; Residues: 238-275 <HOF>
R; Hoffmann, T.; Parr, D.M.
R; Hoffmann, T.; Parr, D.M.
R; Hoffmed to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revisions to residues 25, 59, 60, A; Note: the revised sequence differs from that shown in having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-4 chain C region - human C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change C:Date: 02-Apr-1983 #sequence_revision 02-Apr-1982 #text_change C:Date: 02-Apr-1983 #sequence 02-Apr-1982 #text_change A:Tile: Nuclective sequence of a human immunoglobulin C-gamma-A:Reference number: A90933 MID:83157104 A:Accession: A90933 A:Accession: A90933 A:Accession: A90933 A:Accession: A90933 A:Accession: Aprece was determined from the germline gene R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.2%; Score 1137.5; DB Similarity 94.1%; Pred. No. 5.4e-64; 98; Conservative 8; Mismatches 4
                                    A; Accession: A93132
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Best Local Sim
Matches 208;
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C; Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C; Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C; Accession: A93906; A92809; A90752; A93132; A02148
R; Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con A; Accession: A93906; MUID:82197621
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A;Residues: 1.24,'E', 26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A.Reference number: A92809; MUID:81007873
A.Rotentents: myeloma protein Til.
A.Accession: A92809
A.Molecule type: protein
A.Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A.Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A.Rote: Trp-156 is at or near the complement-binding site
B.Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A.Title: The amino acid sequences of the three heavy chain constant region domains of a A.Title: The amino acid sequences of the A.Title: A.Reference number: A90752; MUID:80001357
A.Reference number: A90752; MUID:80001357
A.Accession: A90752
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                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                            122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240
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                          Residues: 1-377 <HUC> ;Superfamily: immunoglobulin homology
                                                                                                                                                                                                                                                                                            Indels
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                                                                                         C, Keywords: immunoglobulin F; 20-85/Domain: immunoglobulin homology <IMM>
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66.0%; Pre
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nes 227; Conserv
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A; Residues: 1-326 <ELL>
A; Molecule type: DNA
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Matches
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Matches 217; Conservative
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A.Contents: heavy chain disease protein Wis
A.Accession: A90442; MUID:81021548
A.Accession: A90442
A.Accession: A90442
A.Accession: A90442
A.Accession: A90442
A.Accession: A90442
A.Accession: A) And A.Accession: A) A.Accession: 
                                                                                                                                                                                                                                                                                A)Cross-references: GDB:119340; OMIM:147130
A)Cross-references: GDB:119340; OMIM:147130
A)Map position: 14932.33-14932.33
A)Introns: 99/1; 111/1; 221/1
C)Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C, Superfamily: immunoglobulin C region; immunoglobulin c region; immunoglobulin hemology
C, Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma
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                                            constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGO 300
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A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Residues: 12-97 <MIC>
A;Residues: 12-97 <MIC>
a;Note: the hinge region in gamma-3 chains is about four times as long idue segment (12-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F)134-203/Domain: immunoglobulin homology <IM2>
F)240-307/Domain: immunoglobulin homology <IM3>
F)240-3107/Domain: immunoglobulin homology <IM3>
F)140isulfide bonds: interchain (to light chain) #status experiment F:27-83,141-201_247-305/Disulfide bonds: #status predicted F:106,109/Disulfide bonds: interchain (to heavy chain) #status experiF:177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 327;
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                                         Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1e-63;
8; Mismatches
                                 A;Title: Human immunoglobulin sublclasses.
A;Reference number: A90249; MUID:70207560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 92.9
nes 208; Conservative
                                                                                                                                          A; Molecule type: protein
A; Residues: 1-30;81-326 <PIN>
J. 117, 33-47, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;99-110/Region: hinge
                                                                                                        A; Accession: A90249
                                                                                                                                                                                                                                                  A; Gene: GDB: IGHG4
A; Cross references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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A; Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form in R; Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A; Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A; Reference number: A90198; MUID:77021516
A; Contents: heavy chain disease protein Zuc, partial sequence corresponding to residual A; Accession: A90198
                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 59-125, TBF, 128-226,228-289 <WOL>
A; Residues: 59-125, TBF, 128-226,228-289 <WOL>
A; Note: this protein lacks most of the V region, all of the CH1 region, and part of t A; Note: protein lacks most of the V region, all of the CH1 region, and part of t B; A; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deleti A; Contents: heavy chain disease protein 0mm
A; Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A) Molecule type: mRNA A; Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-A; Note: a carboxyl-terminal Lys is removed posttranslationally A; Note: this sequence may represent an allelic form or another gamma chain subclass C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma chain C region - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; A33928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I h A;Reference number: A91749; MUID:84030930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 RIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLIVLHQDWL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 CLKHRSC---PPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAP-CRKHTNCSVFGLLL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Cross-references: GDB:119339; OMIN:147120
A.Map postition: 14402.33-14432.33
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
E.SO3-270.70main: immunoglobulin homology <IMM>
F.303-270.70main: immunoglobulin homology <IMM>
F.317.Wodified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.7%; Score 1125.5; DB 1; 69.6%; Pred. No. 2.7e-63; tive 19; Mismatches 23;
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4:

Gaps

27;

Indels

DB 2;

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Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 1-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Racskovics, I:, Sun, J:, Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUID:95015845
A;Accession: 147159
A;Accession: 147159
A;Molecule type: mRNA
A;Recus: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: 1328 <KAC>
A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
                         A Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residucs: 1-328 < KAC>
A/Residucs: 1-328 < KAC>
A/Cross-references: EMBL:003780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C/Genetics: 1962b
A/Gene: IgG2b
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PSGLYSLSSMVTVPASSLSSKSY------TCNVNHPATTTKVDKRVGTKTK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 PPCP-----APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQPREPQVYILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPCP-----APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGGGTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGGTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPCPICPACESP----GPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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C;Superfamily: immunoglobulin C region; immunoglobulin
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                       39.9%; Score 902.5; DB 2 59.7%; Pred. No. 2.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%; Score 902.5; DB 2
59.7%; Pred. No. 2.3e-49;
tive 36; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Mismatches
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A; Accession: I47160
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Best Local S
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                                                                                                                                                                                                     A,Accession: A90290
A,Molecule type: protein
A,Residues: 1-47, E',49-71, PV',72-128 <PRA>
B,Residues: 1-47, E',49-71, PV', 72-128 <PRA>
F,Martens, C.L.; Moore, K.M.; Steinmetz, M.; Hood, L.; Knight, K.L.
B,Martens, C.L.; Moore, K.M.; Steinmetz, M.; Hood, L.; Knight, K.L.
B,Title: Heavy chain genes of rabbit 196; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Notecule type: mRNA
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic marke B; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
B; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
A; Reference number: A90245
A; McGession: A90245
A; McGession: A90245
A; McGession: A90245
A; McGession: A90245
A; McGeule type: protein
A; Residues: 132-143, 'E', 145-161 <FRU>
A; Residues: 132-143, 'E', 145-161 <FRU>
A; Residues: 132-143, 'B', 145-161 <FRU>
A; Reference number: A94416
                             the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thm
                                                                                                                                      the Fd sections of rabbit immunoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Accession: A94416
A; Accession: A94416
A; Molecule type: protein
A; Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'O', A; Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'O', A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and issulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-82/Domain: immunoglobulin homology <IMI>E; 2130-199/Domain: immunoglobulin homology <IMI>E; 235-303/Domain: immunoglobulin homology <IMI>E; 215-3150-190 immunoglobulin homology <IMI>E; 215-2150 immunoglobulin homology <IMI>E; 2150 immunoglobulin homology <IMI>E; 2150 immunoglobulin homology <IMI>E; 2150
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3555-357, 1994
A;Fitle: Five putative subclasses of swine IgG identified from the cDNA sequences A;Reference number: I47158; MUID:95015845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
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                         A;Note: this sequence has the d12 allotypic marker, R;Pratt, D.M.; Mole, L.E. Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of A;Reference number: A90290; MUID:76135469
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Matches 163; Conservative
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Length 328;

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Job time: 147 sec
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Best Local Similarity
Matches 170; Conserv
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submitted to the Atlas, April 1975
A; Reference number: A94553
A; Molecule type: protein
A; Residues: 1-3 < CRIN.
Biochemistry 10, 18-25, 1971
A; Tile: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A; Reference number: A90352; MUID:71058471
A; Molecule type: protein
A; Reference number: A90352
A; Molecule type: protein
                                                                                                                                                                                                                    ig gamma 4 chain constant region - pig (fragment)
[C] Species: Sus scrofa domestica (domestic pig)
[C] Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
[C] Accession: 147162
[S] RKacsskovics, I , Sun, J.; Butler, J.E.
[A] Title: Five putative subclasses of swine IgG identified from the CDNA sequences of A; Reference number: 147163
[A] Accession: 147162
[A] Status: Preliminary; translated from GB/EMBL/DDBJ
[A] MACCESION: 177162
[A] Status: Preliminary; translated from GB/EMBL/DDBJ
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C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90384; A90385; A02151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGGGTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDLAVEWESNGQ--PENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                       Indels
                                                                               DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.8%; Score 900.5; DB 2
60.6%; Pred. No. 2.5e-49;
tive 35; Mismatches 58
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Best Local S:
Matches 172
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A;Molecule type: protein
A;Residues: 134-226 cmRa>
A;Residues: 13.4-226 cmRa>
Biochemistry 13. 4804-4811, 1974
A;Titchemistry 13. 4804-4811, 1974
A;Titche Primary structure of the C-H3 homology region from guinea pig IgG2 antibodie)
A;Reference number: A90385; MUID:75036073
A;Accession: A9038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Note: Cys-16 is involved in a heavy-light chain bond A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs. C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <a href="https://www.rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/rman.com/r
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Riturner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A.Title: Structure of heavy chain from strain 13 quinea pig immunoglobulin-G(2). II.
A.Reference number: A90359; MUID:71058486
A.Recession: A90359
A.Recession: A90384; J.J.
Biochemistry 13, 4796-4803, 1974
A.Reference number: A90384; MUID:75036072
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F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental
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60.7%; Pred. No. 1.3e-48;
ive 33; Mismatches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: protein
A, Residues: 227-311 <TR2>
R,Ollveira, B.; Lamm, M.E.
Bochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of 9
A, Reference number: A90354; MUID:71058474
A;Contents: annotation; disulfide bonds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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March 1, 2001, 09:17:06; Search time 70.93 Seconds Run on:

(without alignments)
194.760 Million cell updates/sec

JS-09-389-782A-7 Title: Perfect sc Sequence:

2264 1 ETFPPKYLHYDEETSHQLLC......VMHEALHNHYTQKSLSLSPG 404 score:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

268485 seqs, 34193795 residues Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS1/gcgdata/geneseq/geneseqp/AA1980. /SIDS1/gcgdata/geneseq/geneseqp/AA1981.

'/gcgdata/geneseq/geneseqp/AA1990.DAT:* /SIDSI/gogdata/geneseq/geneseqp/AA1996.DAT:*
/SIDSI/gogdata/geneseq/geneseqp/AA1997.DAT:*
/SIDSI/gogdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSI/gogdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSI/gogdata/geneseq/geneseqp/AA1999.DAT:* /geneseqp/AA1994.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	1467	64.8	518	15	R51003	Coar & fo endemos
7	1460	64.5	485	13	R24016	Fusion protein TNF
٣	1332	58.8	376	19	W60037	Antigenic peptide
4	1317	58.2	376	18	W50287	Human Fas antigen
2	1299	57.4	438	16	R81882	Plasmid pDC406/0X4
9	1299	57.4	438	19	W48976	OX40/Fc mutein, C
7	1253	55.3	764	21	Y68949	Fusion protein of
80	1227.5	54.2	375	18	W06683	Herequlin-alpha fu
6	1226	54.2	535	20	X17414	SVPH1-26 disintegr
10	1225	54.1	963	19	W70540	Integrin beta-1 ch
11	1223.5	54.0	664	19	W71603	Human neurturin re
12	1223.5	54.0	664	21	Y80123	Human NTNR alpha a

Rat neurturin rece Rat NTNR alpha and Porcine CTLA-4-IG Human noggin/immun Rabbit TGFbetaRII: Amino acid sequenc	inter inter n poly n poly e LOX-	Humin 11.0 vs alpha Fusion polypeptide Fusion polypeptide Human TGPbetaRII:F Amino acid sequenc ILA. x124D/IGG1 pro Human Interleukin + ICAM/453/IGG immu	Human gpl30-Fc-His Human gpl30-Fc-His Anti-5T4 single ch Aggrecanase artifil Aggrecanase artifil Aggrecanase artifil HUMAN OCR10-Fc fus	Human cytokine rec Human IgG1 hinge/F Human Fc (IgG1). Amino acid sequenc IgG1 hinge, CH2 an Protein from pcd51 Human immunoglobul
W71604 Y80124 Y15123 W96278 W73513	192207 192205 192204 192204 193153 193185	192103 192202 192203 W73514 194064 194461 R48037	W10796 W92184 W86003 W18574 W18575	W31646 W26232 Y06617 Y01372 R89441 Y24154
19 21 20 21 21 21	50055555	21 21 21 21 21 21	20 20 118 21 21	19 18 20 17 17
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## ALIGNMENTS

R51003 standard; Protein; 518 AA.

R51003;

(first entry) 07-0CT-1994

Sequence of a recombinant human (rhu) tumour necrosis factor receptor TNFR/fc fusion protein. 

Tumour necrosis factor receptor; chimeric antibody molecule; immuglobulin.

Synthetic.

WO9406476-A. 31-MAR-1994.

93WO-US08666. 14-SEP-1993;

92US-0946236. 15-SEP-1992;

(IMMV ) IMMUNEX CORP.

Smith CA;

Jacobs CA,

WPI; 1994-118172/14. N-PSDB; Q45225.

Treating TNF mediated inflammatory diseases with TNF antagonist esp. soluble form of TNF receptor, opt. as fusion protein with human immunoglobulin Fc region, esp. for treating arthritis

G1.

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Tumour necrosis factor; TNF; IgG1; immunoglobulin
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                          Q45224 is CDNA from clone 1 of library WI-26 VA4 of human fibroblast cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein baving a mol. wt. of about 75-80 kba.The clohing of the CDNA for TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1 is contained in expression vector pCAV/NOT-TNFR (ATCC 68008). A scontained in expression vector pCAV/NOT-TNFR (ATCC 68008). A crombinant chimeric antibody may be produced having TNFR sequences substituted for the variable domains of either or both of the immunoglobulin molecule heavy and light chains and having unmodified constant region domains. A specific example of a TNFR/FC fission protein is given in Q4525/FS1003. The rub TNFR: Fe fusion protein is given in Q4525/FS1003. The rub TNFR: Fe fusion protein is given in Q4525/FS1003. The rub TNFR: ATCC G8089) conty the cDNA encoding the truncated TNFR. 2) a 700 bp Styl-Spel fragment from plasmid pIXY498 coding for 232 AAS of the CF portion of human IgG1. Plasmid pIXY498 coding for 232 AAS of the CF crost conty. The FC fragment of human IgG1. 3) An oligo linker, to conty the FC fragment of human IgG1. 3) An oligo linker, to linker was created TNF receptor and the 5' end of human IgG1, cend of the truncated TNF receptor and the 5' end of human IgG1, 237. Apriner Q45226, which encodes the 257.237 of human IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 LQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGG---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 pvstrsqhtqptpepstapstsfllpmgpsppaegstgdepkscdkthtcppcpapellg 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eltknqvsltclvkgfyprhiavewesngqpennykttppvldsdgsfflyskltvdksr 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dqvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvck 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GGGGG-----TCPPCPAPELLG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDEETSHOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.8%; Score 1467; DB 15
63.1%; Pred. No. 1.8e-85;
ive 21; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOOGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Disclosure; Page 32-34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 63.19
Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         human IgG1
                                                                                                                                                                                                                                                                                                                                                                                                                                             518 AA;
                                                                                                                                                                                                                                                                                                                                                                                        and primer
257-237 of
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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The sequence is that of fusion protein TNFRFC comprising the extracellular domain of tunnour necrosis factor (TNF) fused via a hinge region to the FC part of the heavy chain of human 1961. It may be used as part of a cell free receptor binding test which can be used for the identification of agonists, antagonists, antibodies, biological activity of soluble cellular receptors, functional analysis of modified ligands and diagnostic or therapeutic substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 dqvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvck 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOYVKOECNRTHNRVCECKEGRYLEI -----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GGGGGGTCPPCPAPELLGGP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 yydq--taqmccskcspgqhakvfctktsdtvcdscedstytqlwnwypeclscgsrcss 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell free receptor binding test contg. recombinant fusion protein comprising carrier bound to fusion partner coupled to fixed support, and second, labelled binding partner, for receptor or antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pvstrsqhtqptpepstapstsfllpmgpsppaedpeepkscdkthtcppcpapellggp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 485;
                                                                                          "human TNF extracellular receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.5%; Score 1460; DB 13;
64.1%; Pred. No. 4.7e-85;
ive 18; Mismatches 83;
                                                                                                                                          "linker and hinge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zettlmeissl G;
                                                Location/Qualifier
                                                                                                                                                                                        "IgG1 CH2"
                                                                                                                                                                                                                                       /note= "IgG1 CH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig 6; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                 91EP-0120187.
                                                                                                                                                                                                                                                                                                                                                                                                                           90DE-4037837
                                                                                                                                                              ..379
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                                                                                                                    253..270
                                                                                                                                                                                                              380..485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BEHW ) BEHRINGWERKE AG.
                                                                                          /note=
                                                                                                                                                                                        /note=
                                                                                                                                               /note=
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening etc.
                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1990;
                                                                                                                                                                                                                                                                                   EP488170-A.
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Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lauffer
                                                                      Region
                                                                                                                    Region
                                                                                                                                                                Region
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R24016 standard; Protein; 485

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(first entry)

26-NOV-1992

EX LX

R24016;

Fusion protein TNFRFC

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Length 376; Indels 119

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120 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGG 179
                                                                                                                                       8 LHYDEETSHQLLCDKCPPGTYLKQHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV; apoptosis modulation; immunoglobulin G1 Fc; 1gG1 Fc; fusion.
                                                                                                                                                                                                                                                                                                                                                        66 CKELQYVKQE--CNRTHNRVCECKEGRYLEIEFCLKHRSCPP----GFGVVQAGTPERNT
                                                                                                                                                                                                                          78 cdeghgleveinctrtqntkcrckpnffcnstvc---ehcdpctkcehgiikectltsnt
                                                                                                                                                                                                                                                                                                                                                                                                              240 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIŞKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                                                                                                                                                                                                                                                                                                     180 GGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYPYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                        58.8%; Score 1332; DB 19; 66.7%; Pred. No. 4.3e-77; ive 15; Mismatches 60;
                                                                                                                                                                                                                                                                                               135 kcke--egsrsnepks---cdk------th--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Fas antigen derivative/IgG1 Fc fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= sig_peptide
17..376
/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1998 (first entry)
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S, Nakamura N;
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09742319-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1997
                                                                          270;
                                          Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                           Best_Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart disease, ischemic restencies of the heart, liver or kidney and endotoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                          Fas ligand; Fas antagonist; apoptosis related disease; liver disease; heart failure; kidney failure; graft-versus-host disease; antibody; myocardial infarction; ischemic restenosis; endotoxic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This represents the antigenic peptide has (nd29) containing the Fc
                                                       TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of Fas antagonist for treatment and prevention of "apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "hFas antigen signal peptide"
                                                                                                                                                                                                                                                                                                                                                                         Antigenic peptide hFas (nd29) containing Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "hFas (nd29) protein"
                                                                                                                                                   377 QGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examples; Fig 5-9; 86pp; Japanese.
                                                                                                                                                                                                                                                            W60037 standard; Protein; 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yatomi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0262521.
96JP-0290459.
96JP-0351718.
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                                                                                                                                                                                                                                                                                                                                       (first entry)
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/note= "]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V34430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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27-DEC-1996;
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07-MAY-1998

Peptide Protein

W60037;

W60037

457

Nagata S,

WPI; 1997-558981/51

N-PSDB; V07004.

376 AA;

Sequence

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W48976
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                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                     CKELQYVKQE--CNRTHNRVCECKEGRYLEIEFCLKHRSCPP----GFGVVQAGTPERNT 119
                                                                                                                                                                                                                                                                                                                                                                     VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 qprepqvytlppsrdeltknqvsltclvkgfypsdiavewesngqpqnnykttppvldsd 330
                                                                                                                                                                                                                                                                                                        8 LHYDEETSHQLLCDKCPPGTYLKQHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65
                                                                                                                                                                                                                                                                                                                     Fas antigen derivative containing modified extracellular region -
has low antigenicity, promotes apoptosis and is useful in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---tcppcpapellggpsvflfppkpkdtlmisptpevtcvvvdvshedpevkfnwyvdg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a Fas antigen derivative/IgG1 Fc fusion, which contains a Fas antigen extracellular region lacking one or more amino acid residues in the region from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                                                                    amino-terminal to (but excluding) the 1st cysteine residue (preferably at least 29 residues are deleted).

The derivative is an effective regulator of apoptosis and can be used (either by administration of the polypeptide, or by the use of the coding DNA in gene therapy) to treat a range of diseases, e.g. diabetes, arthritis, lupus and in particular viral diseases such as hepatitis, influenza and HIV, by modulating apoptosis of virus-infected cells.
                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                      Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pDC406/Ox40/Fc* encoding an Ox40/Fc mutein protein.
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell surface molecule; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gsfflysnltvdksrwqqgnvfscsvmhealhnhytqksls1spg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                     Score 1317; DB 18
Pred. No. 3.9e-76;
; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                             .----th-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pDC406/OX40/Fc*; membrane glycoprotein.
                                               Disclosure; Fig 4; 102pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                          135 kcke--egsrsnepks---cdk----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R81882 standard; Protein; 438
                                                                                                                                                                                                                                                      58.2%;
                         of viral and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytokine;
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                      376 AA;
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Best Local Simil
Matches 267; (
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                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD -- SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                                            This plasmid encodes an OX40/Fc antibody fragment mutein protein, and is used to express a soluble OX40/Fc mutein fusion protein for use in detecting cDNA clones encoding a OX40 ligand. The Fc fragment may be derived from human IgG1, and the plasmid may be used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell line. Cultures supernatant was purified by affinity chromatography and this was used, together with labeled goat anti-human IgG to screen various cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crecqpghqmvnrcdhtrdtlchpcetgfyneavnydtckqctqcnh--rsgselkqnct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- ESTQKSGGGGGGGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEOYNSTYRVVSVLTVLHODWLNGKEY
                                                                                                                                                                                                                                                        New isolated DNA encoding the OX40 ligand polypeptide - also ver
and host cells, used to produce recombinant ligand used in e.g.
prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.4%; Score 1299; DB 16 60.4%; Pred. No. 6.3e-75; iive 22; Mismatches 77;
                                                                                                                                         Goodwin RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCRKHTNCSVFGLLLTQKGNATHDNICSGNS----
                                                                                                                                                                                                                                                                                                                                                   Example 2; Column 35-38; 26pp; English.
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                                                                                                                                         RB,
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                                                                                                                                         Gayle
93US-0097827
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                                                                                                                                       Fanslow WC,
                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                    WPI; 1995-357992/46.
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Matches 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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23-JUL-1993;
                                                                                                                                         Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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431 slslspg 437
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                                                                                                                                                                                                                                                                                          398 SLSLSPG
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                                                                                                       251
                                                                                                                                           278
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 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgG1 antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytckine (W48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 RTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTD--SWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----pgtqprqdsgyklgvdcvpcppghfs--pgnnq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purified polypeptide 0x-40 ligands - for co:stimulation of T-cell production and binding assays for 0x-40 and homologues
                                 cytokine; T cell antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                /note= "Mutant Fc region of human IgGl antibody"
225
                                                                                                                                                                                                                                                                                                           ņ
                                                                                                                                                                                                                                                                                                                                                              "changed from Gly in wild-type to Ala in mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.4%; Score 1299; DB 19; Length 438; 60.4%; Pred. No. 6.3e-75; ive 22; Mismatches 77; Indels 70
                                                                                                                                                                                                                                                   /note= "changed from Leu in wild-type to Ala mutant"
                                                                                                                                                                                                                                                                                                           Gly
                                                                                                                                                                               "Extracellular domain of mouse OX40"
                                                                                                                                                                                                                                                                                                           ಧ
                                                                                                                                                                                                                                                                                                           "changed from Leu in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Col 37-40; 26pp; English.
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gayle RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0494574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0097827
95US-0494574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 60.4
8; Conservative
                                                                                                                                                                                                                                                                                         226
/note= '
                                                                                                                                                                                                                                                                                                                                               228
/note= '
                                                                                          sapiens
                                                                                                                                                              1..206
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-427099/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ptqdtvcrcr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 AA;
                                                                                        - Homo
                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                    Misc-difference
OX40/Fc mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V32636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Sin
Matches 258;
                                                                                      Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baum PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                    chimeric
                                 OX40/Fc;
                                                                                                                                                              Region
                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
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|: |||::| | ackpwinctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvgsttvwprts

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g δ

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Cell development cycle protein of delta family useful for treating various disorders associated with central nervous system e.g. cerebral autosomal dominant ateriopathy and ischemic strokes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a fusion protien of the extracellular domain of a murine polypeptide, which a member of the cell development cycle protein family known as the Delta family of mammalian membrane surface-bound ligands, and the human immunoglobulin G (IGG) Fc portion. The murine delta-related protein gene is expressed
                                                                                                                                                                                         30
11
                                                     277
                                                                                                           KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 337
                                                                                                                                                                                                                                                                                                                                                                                                                             Cell development cycle; Delta family; membrane surface-bound ligand; endothelial cell biology; gene therapy; subcortial infarct; cerebral autosomal dominant ateriopathy; leucoencephalopathy;
                                                                                                                         ---ESTQKSGGGGGGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
               | |:
elpstptlveprscdkt-----htcppcpapeaegapsvflfppkpkdtlmisrtpev
                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein of murine delta-related protein and human IgG Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region of protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "human IgG Fc portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 169-171; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "extracellular delta-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                    Y68949 standard; Protein; 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US15710
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ischemic stroke; chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-195294/17.
N-PSDB; 260926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
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(BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.28;
69.98;
                                                                                                                                                            96WO-US06861.
                                                                                                                                                                               95US-0441863,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                     Aruffo AA, Carlton GW,
  60..375
                                        60..124
                                                                                                                                                                                                                                        WPI; 1997-012095/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AA;
                                                                                                                                                                                                                                                 T45262
                                                                     Cleavage-site
                                                                                                                     WO9636720-A1
                                                                                                                                                            14-MAY-1996;
                                                                                                                                                                               16-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ma
Local S.
246;
                                                                                                                                        21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                  N-PSDB;
  Protein
                                         Region
                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                       15;
       in the control of endothelial cell biology. The murine polynucleotide was identified from a white adipose tissue cDNA library. The polypeptide is useful for identifying receptors, which bind to and/or are activated by the polypeptide. The polynucleotide is useful in gene therapy of cerebral autosomal dominant ateriopathy with subcortial infarcts and leucoencephalopathy, an autosomal dominant disorder causing ischemic
                                                                                                                                                                                                                   gsncekkvdrctsnpcangg-----qclnrgpsrtcrcrpgftgthcelhisdca 446
                                                                                                                                                                                                                                                       r-spcahg-----gtchdlengpvc-tcpagfsgrrcevrithdacasgpcfngatc-- 496
                                                                                                                                                                                                                                                                                                                     PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 244
                                                                                                                                                                                                                                                                                                                               dqensyhcl---cppg-yygqhcehstlt-cadspcfnggscrernggssyacecppnft 396
                                                                                                                                                                                                                                                                              FGLLLTQKGNATHDNIC------SGNSESTQKSGGGGGGGTC 184
                                                                                                                                                                                                                                                                                                                                                           AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 304
                                                                                                                                                                                                                                                                                                                                                                                                QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 364
                                                                                                                                        Gaps
                                                                                                                                                           -- PCPDHYY 49
                                                                                                                                                                                                 "TDSWH-----TSDECLYCSPVCKELQYVKQECNRTHNRVCECKEG-----RYLEIEFCL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "x at position 26 corresponds to an in-frame stop codon in the coding sequence"
                                                                                                                                                                                                                                        KHRSCPPGFGVVQAGT---PERNTVCKRCPDGF-----FSNETSSKAPCRKHTNCSV
                                                                                                                                                                                                                                                                                                                                                                      polypeptides
                                                                                                                                                                                                                                                                                                 ----ytglspnnfvcncpygfvgsrcefpvglppsfpaaaepkscdkt-----htc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor;
                                                                                                                                       Indels 104;
                                                                                                                    Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein; protein phosphorylation; breast cancer; rHRG-alpha-T-Fc.
within vascular endothelium indicates a role for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                        YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                    Score 1253; DB 21
Pred. No. 9.6e-72;
; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heregulin-alpha fusion protein HRG-alpha-T-Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..59
/label= Sig_peptide
/note= "CD5 signal sequence"
                                                                                                                                                           DEETSHOLLCDKCPPGTYLKQHCTAKWKTVCA--
                                                                                                          55,3%; Sc. 58.0%; Pred 22; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W06683 standard; Protein; 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic.
                                                                                                                             Similarity
                                                                                       764 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Homo
Chimeric synth
                                                                                                                    Query Match
Best Local Simi
Matches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-1997
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                    strokes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W06683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       æ
                                                                                                                                                                             342
                                                                                                                                                                                                                   397
                                                                                                                                                                                                                                                                             148
                                                                                                                                                                                                                                                                                                                                                          245
                                                                                                                                                                                                                                                                                                                                                                                                                                        365
                                                                                                                                                           1
                                                                                                                                                                                                 20
                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                          447
                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                            604
                                                                                                                                                                                                                                                                                                                                                                                                 305
                                                                                                                                                                                                                                                                                                                                                                                                                   664
                                                                                                                                                                                                                                                                                                                                                                                                                                                         724
                                                                                                                                                                                                                                                                                                497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clgtsshlvkcae---kektfcvnggec---fmvkdlsnpsr-ylck-cqpgftgarcte 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotic vector encoding growth factor, thrombin cleavage site and human 1gG1 Fc region - esp. encoding EGF-like domain of herequlin-alpha, -beta2 or -beta3, used for prodn. of recombinant fusion proteins capable of HER4 receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rHRG-alpha-T-Fc (W06683) is a fusion protein that incorporates the EGF-11ke binding domain of human herequlin (HRG)-alpha and the Fc portion of human IgG1. It is the product of a cDNA construct (T45262) in vector CDM and can be producted in eukaryotic (esp. COS) host cells. The fusion protein, or the HRG-alpha EGF binding domain produced from it by thrombin cleavage, are both capable of activating human epidermal growth factor receptor 4 (HBR4) and can be used to study receptor functioning, e.g. protein phosphorylation. They are also useful in screening assays for (ant)agonists of HBR3 and HBR4, and bind to cells that express HBR4 e.g. MDA-MB-453 human breast cancer cells, inducing expression of intercellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nvpmkvg------propertygkdpgggggrlvprgfgsgd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fnwyvdgvevhnaktkpreegynstyrvvsvltvlhgdwlngkeykckvsnkalpapiek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                              /note= "mature fusion protein produced following
    signal peptide cleavage"
                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 375;
                                                                                                                                                               EGF-like binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 KAPCRKHTNCSVFGLLTQKGNATHDNICSGNSEST----QKSGGGGG
                                                                                                                                                                                                                                                       142..375
/label= Human Ig-constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.8e-70;
7; Mismatches 44
                                                                                                                                                                                                                            Thrombin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1227.5;
                                                                                                                /label= HRG-alpha
/note= "heregulin-alpha
125.141
/label= Thrombin_cleavao
/label= HRG-alpha-T-Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Culouscou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 7A-B; 188pp; English.
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535 AA;

Sequence

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oplypeptides are proteinases implicated in fertilisation and spermatogenesis. They can be used as therapeutic agents. A proteinase inhibitor of the catalytic domain would inhibit SyPH1-26 activity and would be useful as a method for birth control. Also, an inhibitor of the catalytic domain object fertilisation. The proteinase disintegrin domain of SyPH1-26 may affect fertilisation. The proteinase activity of SyPH1-26 can also be used as a detergent additive for the removal of stains having a protein component. The SyPH1-26 polypeptides and fragments can also be used as molecular weight markers, as markers for determination of isolectric points of sample proteins and as controls for establishing the extent of fragmentation of a protein sample. The products can also be used for identifying, separating or sample. The products can also be used for identifying, separating or purifying cells that express SyPH1-26 polypeptides such as testis cells. The present sequence represents a fusion protein from an example of the present invention comprising; the IG Kappa signal sequence at positions 1 to 20; a spacer at positions 21 to 22; the SyPH1-26 disintegrin domain at positions 308 to 535.
                                                                                                                                                                                                                SVPH1-26 disintegrin domain, Ig kappa signal, Fc IgG1 fusion protein.
                                                                                                                                                                                                                                             Human, SVPH1-26, proteinase, testis, fertilisation, spermatogenesis, birth control, detergent additive, diagnosis; testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human SVPH1-26 DNA useful for the diagnosis and prognosis of testicular cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human SVPH1-26. Human SVPH1-26
               353 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                /label= spacer
23.1305
//note= "SVPH1-26 disintegrin domain"
306.1307
                                                                                                                                                                                                                                                                                                                                                                                  /note= "Ig kappa signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= spacer
308.535
/note= "IgG1 Fc domain"
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 59; 96pp; English.
                                                                                                              Y17414 standard; Protein; 535 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0063571.
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-337487/28
                                                                                                                                                                                                                                                                                                 Homo sapiens,
Synthetic,
                                                                                                                                                                               26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09923228-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1999
                                                                                                                                              Y17414;
                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                              323
                                                                               RESULT
                                                                                                Y17414
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14;
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Inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
                                                                                                                                                                                                                             234 irkkcasmvhlsgacgpktcnmrgicn-----nkgh---chcnhewappyckdkg 280
                                                                                                                                                                                                                                                                                                                       54 lhpgaacafgicckdckflpsgtlcrqqvgecdlpewcngtshqcpddvyvqdgiscnvn 113
                                                                                                                           114 afcyektcnnhdiqckeifgqdarsasqscyqeintqgnrfghcgivgttyvkcwtpdim 173
                                                                                                                                                     -----EFCLKHRSC-----PPGFGVVQAGT---PERNT 119
                                                                                                                                                                             174 cgrvqcenvgvipnliehstvqqfhlndttcwgtdyhlgmaipdigevkdgtvcgpeiic 233
                                                                                                                                                                                                                                                                                                                                                             WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF 330
                                                 8 LHYDEETSHQLLCDKC---PPGTYLKQ---HC-TAKW-KTVCAPCPDHYYTDSWHTSDEC 59
                                                                                                                                                                                                       120 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSE-----STQKS
                                                                                                                                                                                                                                                         -----TCPPCPAPELLGGPSVFLFPPKPKDTLM
                                                                                                                                                                                                                                                                      211 ISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                          Indels 110;
                                                                                                   60 LYC-----SPVCKEL-----QYVKQECNRTHNRV--CECKEGRYLEI---
  Length
Score 1226; DB 20;
Pred. No. 3.3e-70;
                       18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..20
/note= "signal peptide"
21..963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W70540 standard; Protein; 963 AA.
54.28;
54.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-JP00370
                         Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 HNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Integrin beta-1 chain.
                                                                                                                                                                                                                                                        175 GGGGGGG-----
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9832771-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W70540;
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                                                                                                                                                                                                                                                                                                                                                           271
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RESULT
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                                                                                                                                                                                                                                                                                     This represents an integrin beta-1 chain. The invention provides integrin-immunoglobulin chimeric protein heterodimer complexes that complians alpha or beta chain associated with an integrin alpha chain and confidence confidence complexes. In particular with a chimeric proteins form heterodimer complexes, in particular with a chimeric protein containing an integrin beta chain and an immunoglobulin chain, at the immunoglobulin chain, and an immunoglobulin chain; the immunoglobulin chain. The integrin alpha chain is preferably alpha 4 two may be a light chain. The integrin alpha chain is preferably alpha 4 transformed with vectors containing the DNA coding for the above chimeric proteins can be used in the preparation of the chimeric proteins and their heterodimer complexes. The heterodimer complexes, which are useful for testing potential promoters and inhibitors of the binding of integrins to thair ligands, function as blood platelet substitutes and integrin agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TNCSVFGLLLT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 --vck-ctdpkfggqtcemcqtclgvcaehkecvqcrafnkgekkdtctqecsyfnitkv 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKGNATHDNI------169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |:
| 134 kscdkt-----htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshed 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRTHN-------GFGVVQAGTPER 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      esrdklpqpvqpdpvshckekdvddcwfyftysvngnnevmvhvvenpecptgpedpeep 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ETFPPKYLHYDEETS--HQLLCD------KCPPGT-----YLKQHC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 TAKWKTVCAPCPDHY-----YTDSWHTSDECLYCSPVCKELQYVKQ------EC 76
                                                                                                                                                               Integrin-immunoglobulin chimeric protein heterodimer complexes as platelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | | : : | | ecstdevnsedmdaycrkensseicsnngecvcgqcvcrkrdntneiysgkfcecdnfnc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 drsnglicggngvckcrvcecnpnytgsacdcsldtstceasnggicngrgicecg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -STQKSGGGGGGGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.1%; Score 1225; DB 19
50.4%; Pred. No. 7.4e-70;
ive 31; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 NTVCKRCPDGFFSNETSSKAP----CRKH----
                                                                                                                                                                                                                                                       Claim 9; Pages 50-57; 87pp; Japanese.
                                                                                                                                                                                                                        presence of plasma components
97JP-0015118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                    (TORA ) TORAY IND INC
                                                                        Kainoh M, Tanaka T;
                                                                                                          WPI; 1998-427881/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 AA;
                                                                                                                           N-PSDB; V33773
29-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim
Matches 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
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The present sequence represents human neurturin receptor alpha

(NTNR-alpha)/FC sequence (IfF2a) fusion protein, from an example of the present invention. WINR-alpha proteins can be used: (a) to identify molecules that bind specifically to it (potential agonists and antagonists) and to purify such compounds: (b) to modulate response of cells to neurturin (NTN); (c) to increase survival of Ret-expressing cells or to activate Ret on the surface of cells (soluble glial derived neurotrophic factor receptor (GDNFR alpha) may be used the same way); (d) to increase the half-life of cognate ligands (soluble glial derived adminant feed additive or molecular weight marker. NTNR-alpha, its genes, animal feed additive or molecular weight marker. NTNR-alpha, its genes, animal feed additive or molecular weight marker. NTNR-alpha, its genes, cant) agonists and antisense nucleic acids, are useful in vivo or ex vivo for treating conditions related to abnormal NTN activity or response, particularly neurological (central or enteric), renal or haematopoietic (spleam) diseases or injuries. Ab may be agonists or antagonists for therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-alpha expression, e.g. in some tumours), also reagents for immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; neurturin receptor alpha; NTNR-alpha; variant; chimeric;
fusion protein; immunoadhesion; ret-expressing cell; neurological;
renal; haematological disease.
                                                                                                                                                                                                                                                                                                                                                                                         Human neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide(s) based on human neurturin receptor alpha and related nucleic acid - useful for increasing survival of ret-expressing cells for treating e.g. neurological, renal and haematological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Indels
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62.1%; Pred. No. 6e-70;
iive 24; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 81-83; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A;
                                                                                                                                                                                              AA
                                                                                                                                                                                          W71603 standard; Protein; 664
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97US-0802805.
97US-0871913.
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                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-467175/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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18-FEB-1997;
09-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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Best Local Si
Matches 260;
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                                                                                                                                                                                                                                                          W71603;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a neurturin receptor alpha (NTNR alpha). NTNR alpha binds neurturin. The NTNR alpha nucleic acid molecule is useful for the expression of NTNR alpha, which may be used to identify agonist and antagonist compounds having therapeutic applications, such thrombocytopaenia, hypoplasia, treating anaemia, thrombocytopaenia, hypoplasia, or haemorrhage. The present sequence is a NTNR alpha and IgG (immunoglobulin G) fusion protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino acid sequence excluding the N\text{-terminal} signal peptide -
                                                                         165
                                                                                                                       225
                                                                                             379 ekt---pslpddlsdstslgtsvittctsvqeqgl----kannskelsmcftelttniip 431
                                                                                                                                  HEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 285
                                                                                                                                                                                            544
                                                                                                                                                                                                                   LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 345
                                                                                                                                                                                                                                346 ENNYKITPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                                               Human; neurturin receptor alpha; NTNR alpha; splenic haematopoiesis; anaemia; thrombocytopaenia; hypoplasia; haemorrhage.
                         --RSCP--PGFGVVQAGTP
                                     ERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHD------NICS
                                                                                                                     166 GNSESTQKSGGGGGGGGCTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
274 ncrasyqtvts-cpadnyqaclgsyagmigfdmtpnyvdssptg---ivvspwc--
                                                                                                                                                                                                                                                                                                                                                                                                                           Human NTNR alpha and IgG fusion protein SEQ ID NO:16.
                       KQECNRTHNRVCECKEGRYLEIEF----CLKH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Column 91-96; 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein
                                                                                                                                                                                                                                                                                                                                                   Y80123 standard; Protein; 664
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                           Y80123;
                                                                                                                                                                                                                                                                                                                             RESULT 12
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LPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 345
                                                                                              73 KQECNRTHNRVCECKEGRYLEIEF----CLKH------RSCP--PGFGVVQAGTP 115
                                                                                                                                           cs 165
                                                                                                                                                                                                  ip 431
                                                                                                                                                                                                                        VS 225
                                                                                                                                                                                                                                                                      VKA 285
                                                                                                                                                                                                                                                                                    dvs 484
                                                          Gaps
                                                                                ----YTDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                  ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
                                                                                                                                                                                                                                                                                                                                                                                         663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurturin receptor alpha; NTNR-alpha; variant; chimeric; protein; immunoadhesion; ret-expressing cell; neurological;
                                                                                                                                                                                                                                                                                                                                                                            Rat neurturin receptor alpha/Fc sequence (IfF2a) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide(s) based on human neurturin receptor alpha and related nucleic acid – useful for increasing survival of
                                                                                                                                                                                           |: | | | : : | | | | 379 ekt---pslpddlsdstslgtsvittctsvqeqgl----kannskelsmcftelttf
                                                                                                                                                                                                                                     | : |: |-----htcppcpapellggpsvflfppkpkdtlmisrtpevtcvvv
                                                                                                                                                                                                                                                                      HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV$
                                   66
                                                                                                                                                                                                                        GNSESTQKSGGGGGGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                           116 ERNTVCKRCPDGFFSNETSSKAPCRKHINCSVFGLLLTQKGNATHD-----
                                   Length
                                                          Indels
                                   21;
                                                         ,09
                                   DB
                                 Score 1223.5; Di
Pred. No. 6e-70;
; Mismatches (
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                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haematological disease.
                                                                                HCTAKWKTVCAPCP-DHY -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 W71604 standard; Protein; 664
                                  54.0%;
62.1%;
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97US-0802805.
97US-0871913.
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
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                                              Similarity
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664
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18-FEB-1997;
09-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9836072-A1
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                                                         260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                 Query Match
Best Local S
Matches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W71604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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The present sequence represents rat neurturin receptor alpha (NTMR-alpha)/FC sequence (IFT2a) fusion protein, from an example of the present invention. NTNR-alpha proteins can be used: (a) to identify molecules that bind specifically to it (potential agonists and antagonists) and to purify such compounds; (b) to modulate response of cells to meutrurin (NTN); (c) to increase survival of Ret-expressing cells or to activate Ret on the surface of cells (soluble glial derived neurotrophic factor receptor (GDNFR alpha) may be used the same way); (d) to increase the half-life of cognate ligands (sepecially NTN); (e) animal feed additive or molecular weight marker. NTNR-alpha, its genes, animal feed additive or molecular weight marker. NTNR-alpha, its genes, cartlagonists and antisense nucleic acids, are useful in vivo or ex vivo for treating conditions related to abnormal NTN activity or response, particularly neurological (central or enteric), renal or haematopoietic (splean) diseases or injuries. Ab may be agonists or antagonists for therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-alpha expression, e.g. in some tumours), also reagents for immunoassay and affinity purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 KQECNRTHNRVCECKE-------GRYLEIEFCLKHRSCPPGFGVVQAGT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ncrgsgnmeeecekflrdftenpclrnaigafgngtdvnmspkgpslp----atgapr 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGNSESTQKSGGGGGGGGTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YTDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; neurturin receptor alpha; NTNR alpha; splenic haematopoiesis; anaemia; thrombocytopaenia; hypoplasia; haemorrhage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 alpapiektiskakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 664;
ret-expressing cells for treating e.g. neurological, renal and haematological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat NTNR alpha and IgG fusion protein SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1221.5; DB Pred. No. 8e-70; 24; Mismatches (
                                                               Example 3; Page 84-86; 116pp; English.
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61.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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The present invention describes a neurturin receptor alpha (NTNR alpha). NTNR alpha binds neurturin. The NTNR alpha nucleic acid molecule is useful for the expression of NTNR alpha, which may be used to identify agonist and antagonist compounds having therapeutic applications, such as enhancing splenic haematopoiesis, treating anaemia, thrombocytopaenia, hypoplasia, or haemorrhage. The present sequence is a NTNR alpha and 196 (immunoglobulin G) fusion protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino acid sequence excluding the N-terminal signal peptide \dot{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 KQECNRTHNRVCECKE--------GRYLEIEFCLKHRSCPPGFGVVQAGT 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| | ::|; : || | |:|
274 ncrasyrtits-cpadnyqaclgsyagmigfdmtpnyvdsnptg---ivvspwc-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 8e-70;
24; Mismatches
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61.0%; Pred. No. 8e-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 HCTAKWKTVCAPCP-DHY-----
                                                                                                                                                                                                                             97US-0957063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Z91460
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                                                                                                                                                            15-FEB-2000
Rattus sp.
Synthetic.
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The present sequence is porcine CTLA-4-Ig construct for xenograft -specific immunosuppression. In a pig-to-human transplantation, the soluble protein could comprise the extracellular domain of porcine CTLA-4 fused to a human C gamma I chain of IgG1. This construct was subcloned into the expression vector pHOOK-3TM and used to transfect DAP.3 or CHO-KI cells. PCTLA-4-Ig preferentially binds to porcine B7 and blocks its interaction with CDSB on recipient T-cells. This is useful as a species-specific reagent to inhibit human T-cell proliferative responses to a variety of stimulators.
                                                                                                                                                                                                              Porcine CTLA-4; soluble protein; xenograft; organ transplant; B7; CD28; xenograft-specific immunosuppression; recipient T-cell; anergy; co-stimulatory signal 2; homology; human CTLA-4; bovine CTLA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting T-cell mediated rejection of xenotransplanted organs
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/note= "Denotes the junction between pCTLA-4"
169..362
/label- IgGl_domain
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                                                                                                                                          Porcine CTLA-4-Ig construct
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53.9%; Score 1220.5; DB 389.5%; Pred. No. 5.2e-70; ive 2; Mismatches 14;

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Query Match Best Local S: Matches 231;

156

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DB 21; Length 400;

LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 326 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 386 

267

327

HEALHNHYTOKSLSLSPG 404

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March 1, 2001, 09:20:11 ; Search time 135.68 Seconds
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346.406 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-389-782A-8 2246 1 MDKTHTCPPCPAPELLGGPS......QKGNATHDNICSGNSESTQK 401

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

374700 seqs, 117207915 residues Searched:

374700 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_15:* Database :

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_plant:* sp_rodent:* sp_fungi:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		,			COLUMNIA	
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	1009	44.9	401	4	000300	000300 homo sapien
7	1008	44.9	372	4	Q9UHP4	Oguhp4 homo sapien
m	888	39.5	401	11	008712	008712 mus musculu
4	875	39.0	401	11	008727	008727 rattus norv
S	824.5	36.7	437	11	Q9R1A4	O9rla4 mus musculu
9	433	19.3	300	4	095407	095407 homo sapien
7	405.5	18.1	302	13	09PUS0	OgpusO salvelinus
∞	332.5	14.8	459	11	062327	062327 mus musculu
6	331	14.7	439	4	016042	016042 homo sapien
10	327	14.6	482	11	088734	O88734 mus musculu
11	287	12.8	655	4	075509	075509 homo sapien
12	276	12.3	384	4	Q9UP60	Ogup60 homo sapien
13	272.5	12.1	684	13	090544	090544 ginglymosto
14	271	12.1	416	4	O9NPP6	Ognop6 homo sapien
15	252.5	11.2	616	4	09Y6Q6	O9veq homo sapien
16	252.5	11.2	625	11	035305	035305 mus musculu
17	234.5	10.4	348	12	057103	O57103 monkeypox v
18	233.5	10.4	349	12	057099	O57099 monkeypox v
19	231.5	10.3	349	12	057291	057291 monkeypox v

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# ALIGNMENTS

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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                              OSTEOPROTEGERIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                           Matches 173; Conservative
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                                   01-OCT-2000 (TremBLrel
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                                                            Homo sapiens (Human),
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Best Local Similarity
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                      osteoprotegerin/osteoclastogenesis-inhibitory factor.";
Eur. J. Biochem. 254:685-691(1998).
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
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                                                                   SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
                                                                                                     -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICTY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL: ABO02146; BAA25910.1: -
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                                                          OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
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Pred. No. 3.7e-80;
1; Mismatches 0; Indels (
Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
          "Cloning and characterization of the gene encoding human
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EB42FA51C9D7C71E CRC64;
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CHAIN 22 401 OSTEOPROTEGERIN.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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BY SIMILARITY.
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PFAM; PF00020; TNFR_C6; 3.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PRODOM; PD000771; -: 1.
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**09UHP4** 

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Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
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MEDLINE-97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sulliyan
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                        ביימון wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                         He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.; "Cloning and Expression of Osteoprotegerin from Homo sapiens."; Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999). HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    008712; 070202;
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last snotation update)
01-JUL-2000 (TrEMBLrel. 15, Last annotation update)
03TEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
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                  13, Last sequence update)
15, Last annotation update)
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100.0%; Pred. No. 4.2e-80;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001368; -.
PFAM; PF00020; TNFR_c6; 3.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
NON_TER 1 1
SEQUENCE 372 AA; 42758 MW; F02527A5CDI
Created)
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MEDLINE-98382527; Pubmed-9714833;
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SEQUENCE FROM N.A.
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141 VCKKCPDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNVCSGNREATQK 194
                                                                                348 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK
             21
                                    288
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                                                                          SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTBOCLASTOGRNESIS BY INTERUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTBOCLAST PROGENITORS.
STROMAL CELLS AND OSTBOCLAST PROGENITORS.
SUBCELLUIAR LOCATION: EXTRACELLUIAR.
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
PLACENTA. NOT DETECTED IN SPLEEN.
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
15 TO DAY 17.
         Higashio K.;
"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
"Structure of the mouse osteoclastogenesis.";
gene and its expression in embryogenesis.";
Gene 215:339-343(1998).
-1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMINATION OF NEWLY
Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.
                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U943131; AAB53708.1; --
EMBL; AB013893; BAA28269.1; --
EMBL; AB013909; BAA33388.1; --
EMBL; AB013909; BAA33388.1; --
EMBL; AB013909; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013901; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
EMBL; AB013902; BAA33388.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> P (IN STRAINS 129/OLA AND NIH
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INTERPRO; IPR00488; -.
INTERPRO; IPR00188; -.
INTERPRO; IPR001368; -.
PROSITE; PS00623; TNFR_C66; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS5000711; -; 1.
Glycoprotein; Repeat; Cytokine; Signal.
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TNFR-CYS 3.
TNFR-CYS 4.
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Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Osteoprotegerin: a novel secreted protein involved in the regulation
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Repeat; Cytokine; Signal.
SIGNAL 1 21 BY SIMILARITY.
2 401 OSTEOPROTEGERIN
DOMAIN 23 201 4 X TNFR-CYS.
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BY SIMILARITY.
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POTENTIAL.
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TNFR-CYS 2.
TNFR-CYS 3.
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PFAM.
PFONDITE; PSO0652; TNFR_OG; 4.
PROSITE; PSO0652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PRODOM; PD000771; -; 1.
                    01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                         MEDLINE=97262071; PubMed=9108485;
                                                                                                                                                                                                                                                                                                                                                         EMBL; U94330; AAB53707.1;
HSSP; P25942; 1CDF.
 PRELIMINARY;
                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
365
365
62
80
97
142
160
165
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                               TISSUE-INTESTINE;
                                                                      INFRSF11B OR OPG.
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CARBOHYD
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15; Indels

Length 401;

Score 888; DB 11; Pred. No. 1.4e-69;

Score 888;

39.5%; 86.8%;

8; Mismatches

Matches 151; Conservative

Local Similarity

Query Match

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SEQUENCE
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"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scPt).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
BEMBL, AF152372; AAD40243.1;
HSSP; PO18422; 7FAB.
INTERPRO; IPR003006;
PFAM; PF00047; ig; 4.
PROSITE: PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                      228 KETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                        36.7%; Score 824.5; DB 11; Length 437; 62.9%; Pred. No. 5.2e-64; ative 43; Mismatches 35; Indels 5;
                                                                                                                                                                                                                                                                                                                                   VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQ
                                                                                                                                     Indels
                                      46192 MW; FEC6A31F1D4E573A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
                                                                                              ; Score 875; DB 11;
; Pred. No. 1.8e-68;
10; Mismatches 15;
  POTENTIAL
                      POTENTIAL
                                                                                              39.0%;
85.5%;
                                                                                              Query Match
Best Local Similarity 85.5%
Matches 148; Conservative
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401 AA;
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437 AA;
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Best Local S
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SEQUENCE FROM N.A.
MEDLINE=99087326; PubMed=9872321;
MEDLINE=99087326; PubMed=9872321;
Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
Goddard A.D., Botstein D., Ashkenazi A.;
"Genomic amplification of a decoy receptor for Fas ligand in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 PIYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V. Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.; "Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BLOOD;
MEDLINE-9253915; PubMed=10318773;
Yu R.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
Yu R.Y., Identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Blol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AA; 32679 MW; F90AEE33718449AF CRC64;
                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A. 97:1230-1235(2000).
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42.9%; Pred. No. 4.9e-30;
tive 29; Mismatches 63
300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00020; TNFR_c6; 4.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS50050; TNFR_NGFR_2; 2.

PRODOM; PD000771; -; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20122600; PubMed=10655513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cluster.";
Proc. Natl. Acad. Sci. U.S.A. 97
EMBL; AF104419; AAD296681; -.
EMBL; AF217796; AAF352441; -.
EMBL; AF217793; AAF338851; -.
EMBL; AF217794; AAF338851; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 396:699-703(1998).
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P25942; ICDF.
INTERPRO; IPR000561; -.
INTERPRO; IPR001368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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PRT;
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yctokine 2:231-237(1990).
EMBL; S63368; AAB19824-1; --
HSSP; P25942; ICDF.
                                                                                                                                                   14.8%; Scor
38.3%; Prec
PS00652; TNFR_NGFR_1;
PS50050; TNFR_NGFR_2;
                                                                                                                  48686 MW;
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                          87
93
268
345
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                                          87
93
268
345
421
459 AA;
                                                                                                                                                                          Similarity
                                                                                                                                                                                      64;
                                                      VARIANT
VARIANT
VARIANT
VARIANT
SEQUENCE
             PROSITE;
NON_TER
VARIANT
                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                       Matches
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                                                                                                                                                                                                         SEQUENCE FROM N.A.

BODE J., GOETZ F.W.;

BODE J., GOETZ F.W.;

A tumor necrosis factor receptor homolog is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";

Biol. Reprod. 0:0-0(1999).

BMBI; ARIS6738; AAD56428.1; -.

HSSP; P19438; 1EXT.

INTERPRO; IPRO00561; -.

INTERPRO; IPRO01368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 DEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 YVKQECNRTHNRVCECKEGRYL -- EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salvelinus fontinalis (Brook trout).

Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     302 AA; 34037 MW; E44C73477F05C3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%; Score 405.5; DB 13;
45.2%; Pred. No. 1.2e-27;
tive 30; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 FSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 YSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCA 182
                                        302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 AA.
                                                                                                                                                                                                                                                                                                                                            PFAM; PF00020; TNFR_c6; 4.

PROSITE; PS00622; TNFR_MGFR_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                     Created)
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                                        PRT;
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EMBL; X76401; CAA53981.1; -.
HSSP; P19438; 1NCF.
                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-0CT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO01368; -. PFAM; PF00020; INFR_C6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 45.29 tes 71; Conservative
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                             DECOY RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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          RESULT
Q9PUSO
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237 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 LQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGTPERNTVC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 YIDSWHISDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRS 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-91370690; PubMed-1966549;
Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
Brockhaus M., Lesslauer W.;
"Two human TNF receptors have similar extracellular, but distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 KRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S -> T.

F -> I.

F -> I.

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C51D2CF1C4626DF CRC64;
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PRAM; PF00020; TNFR_C6; 4
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
PRODOM; PD000771; -: 1.
SEQUENCE 439 AA; 46090 MW; FEBCBE329CC67FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR.
                                                                                                                                                                                                                           Score 332.5; DB 11;
Pred. No. 4.8e-21;
0; Mismatches 70;
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235 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 YRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 PWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 KELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Zheng S., Cao J., Cao W., Cai X., Geng L.; Zheng S., Cao J., Cao W., Cai X., Geng L.; "Identification and characterization of SNC73, a gene which is down-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.8%; Score 287; DB 4; Length 65 35.4%; Pred. No. 6.9e-17; ive 21; Mismatches 81; Indels
                                                 SEQUENCE FROM N.A.

Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J.,
Vincenz C., Aggarwal B.B., Dixit V.M.;
"Identification and functional characterization of DR6,
domain-containing TNF receptor.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            Parker A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF068868; AAC34583.1; -.
EMBL; AL096801; CAB75692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulated in colorectal cancer.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF10574-20; AAC19365.1; --
HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                               48939391C4852A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1.
WW; BA7ADC3CA5A9DD48 CRC64;
Eutheria; Primates; Catarrhini; Hominidae;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                HSSP; P07174; INGR.
INTERPRO; IPR000488; -
INTERPRO; IPR001368; -
PFAM; PF00020; TNFR_6; 4.
PFAM; PF00531; death; 1.
PR0SITE; PS00052; TNFR_NGFR_1; UNI
PROSITE; PS50017; DEATH_DOMAIN; 1
PROSITE; PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               71844 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR003006; -. PFAM; PF00047; ig; 3. PROSITE; PS00290; IG_MHC; SEQUENCE 384 AA; 40947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.8%
Best Local Similarity 35.4%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                PRODOM; PD000771; -; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 AA;
                                                                                                                                                                             SEQUENCE FROM N.A.
                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (Tr
01-OCT-2000 (Tr
SNC73 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UP60
Q9UP60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q9UP60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPKY-----LHYDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 CKELQYVKQECNRTHNRVCECKEGRYLEIEF-----CLKHRSCPPGFGVVQAGTPERN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
"The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure and
Characterization of the two Transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LWVALVFELQLWATGHTVPAQVV------LTPYKP--EPGYECQISQEYYDR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       075509;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 18, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
THER RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (THER-RELATED DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ETSHQLLCDKCPPGTYLKQHCT-----AKWKTVCAPCPDHYYTDSWHTSDECLYCSPV
                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 TVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51106 MW; F6C15046B48FF83C CRC64;
                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 327; DB 11; 32.6%; Pred. No. 1.5e-20; ive 25; Mismatches 88;
                                                                                                                                        482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 AA
                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X14619; CAA74969.1; --
EMBL; X14620; CAA74969.1; --
EMBL; X14621; CAA74969.1; JOINED.
EMBL; X14622; CAA74969.1; JOINED.
EMBL; X14623; CAA74969.1; JOINED.
EMBL; X14679; CAA74969.1; JOINED.
HSSP; P19438; INCF.
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00020; TWFR_C6; 4.
PROSTIE; PS0052; TWFR_NGFR_1;
PROSTIE; PS50050; TWFR_NGFR_2;
PRODOM; PD000771; -; 1.
                                                                                                                                                                  01-CCT-2000 (TrEMBLrel. 08, Li
01-CCT-2000 (TrEMBLrel. 15, La
PRO THF-ALPHA RECEPTOR.
TNFR2.
Mus minor
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.69
Matches 75; Conservative
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001368; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 AA;
                                                                                                                                                                                                                                                                                                                                                       N.A.
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DR6 OR DJ181J13.1.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
              396
                                   :|: |
177 VCTSTS 182
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
              ICSGNS
                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics
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                                                                                                                                    088734
088734;
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                                                                                                   RESULT 10
              391
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075509
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384 AA

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Gaps

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Length 655;

Length 384;

DB 4;

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196 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, IMMUNOGLOBULIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 32.8%
Matches 77; Conservative
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFRSF11A OR RANK.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                           9ddN60
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                                                                                             9ddN60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ′;
               10;
                                                                                                                                                                                                                    294 RWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKTTPPVLDSDGSFFLYSKLTVDK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAV 160
                                                                                                                                                               161 EWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 215
                                                                                           42 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 101
               Gaps
                                                                 119 KHYTNPSQDVTVPCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLLLGSEANLT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A new antigen receptor gene family that undergoes rearrangement and
                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 01, Last sequence update)
NOVEL ANYIGEN RECEPTOR PRECURSOR.
Ginglymostoma cirratum (Nurse shark).
Eldsmyotta, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Ginglymostomathii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 684;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
2FF9D2071CDA6DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
Pred. No. 3.3e-16;
; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extensive somatic diversification in sharks.";
Nature 374:168-173(195).
HEMBL; U18701, ARB48195.1; -.
ARBSP; P01867; IFC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-15
                                        3 KTHTCP-----PCPAPELLGGPSVFLFPPKPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Score 272.5; 33.3%; Pred. No. 1.36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Mismatches
                                                                                                                                                                                                                                                                                                                                                   684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047; ig; 6.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=SPLEEN;
MEDLINE-95183140; Pubmed=7877689;
               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 684 NW;
 31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Conservative
               Conservative
                                                                                                                                                                                                                                                       216 HYTQKSLSLSPGKET 230
                                                                                                                                                                                                                                                                                354 AFTOKTIDRLAGKPT 368
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             684 AA;
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 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                 Q90544
Q90544;
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                                                                                                                                                                                                                                                                                                                        RESULT 13
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62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 GQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSOELPREKYLTWASR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The European IMAGE consortium for integrated Molecular analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 QEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 LD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKET 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 271; DB 4; Length 416; 32.8%; Pred. No. 1e-15; ive 34; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389978; CAB97534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                  MBLrel. 15, Last sequence update)
MBLrel. 15, Last annotation update)
HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                      Ä
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635 AEWNSDTTYSCLVGHPSL-NRDLIRSTNKSNGK
                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                  PRT;
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                           305 NRTHNRVCECKEGRY--LEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETS 362
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TURR-CYS 2.

TURR-CYS 4.

BY SIMILARITY.

BY SIMI
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EMBL; AF018253; AAB86809.1; -.
HSSP; P25942; 1CDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THTERENC: IPRO01368; -.
PFAM: PF00020; TNFR_C6; 4.
PROSITE; PS0052; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
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Search completed: March 1, 2001, 09:20:13 Job time: 411 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 1, 2001, 09:17:48 ; Search time 40.97 Seconds
 (without alignments)
316.083 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-389-782A-8
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1 MDKTHTCPPCPAPELLGGPS.....QKGNATHDNICSGNSESTQK 401

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 88757 seqs, 32294092 residues Searched:

88757

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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HVC2_HETFR	ALC_RABIT	HVCS_HETFR	MUC_CHICK	CD40_MOUSE	HVC3_HETFR	HVCM_HETFR	HVC1_HETFR	ALC1_HUMAN	ALC1_GORGO	ALC2_HUMAN	CD40_HUMAN
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303	299.5	293.5	287.5	284	282.5	278.5	278	276	271.5	271	264
34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Homo sapiens (Human)
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330 AA;
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                                                                                                                    Deisenhofer J.;

"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Biochemistry 20:2361-2370(1981).

-!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KoL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.
-!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES.
-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES.
-!- MISCELLANEOUS: BU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES.
                          MEDLINE=77070267; PubMed=1002129; Deteker L., Schwarz J., Reichel W., Hilschmann N.; Rerker L., Schwarz J., Reichel W., Hilschmann N.; Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                 MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
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PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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MEDLINE=81208100; Pubmed=7236608;
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HINGE.
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Biochemistry 9:3188-3196(1970).
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PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"The primary structure of a human IgG2 heavy chain: genetic,
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Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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100.0%; Pred. No. 1.2e-78;
ive 0; Mismatches 0;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2 CHAIN C REGION.
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Best Local Similarity 100.
Matches 227; Conservative
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Eur. J. Blochem. 228:886-893(1995).
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                            SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDIJNE-80001357; PubMed-113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human igGz myeloma protein.";
Can. J. Blochem. 57:758-767(1979).
                                                                                         SEQUENCE OF 238-275 (ZIE).

MEDLINE-80114419, PubMed=118920;

Hofmann T., Parr D.M.;

A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";

Mol. Immunol. 16:923-925(1979).
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INTERPRO; IPR003006; -
PFAM; PF00047; 4g; 3.
PROSTITE; PS000290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
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evolutionary, and functional implications."; J. Immunol. 125:1048-1054(1980).
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                                                                                                                                                            [5] REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
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Submitted (MAR-1980) to the PIR data bank.
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EMBL; V00554; CAA23815.1; -.
EMBL; V00554; CAA23816.1; -.
EMBL; V00554; CAA23817.1; -.
PIR; AO2148; GZHU.
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Fluman immunosplobulin subclasses. Partial amino acid sequence of constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83157104; PubMed-6299662;
Ellison J.W., Buxbaum J.N., Rood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
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                                                                                                                                                    Score 1142.5; DB 1;
Pred. No. 2.1e-72;
8; Mismatches 4;
/FTId=VAR_003889
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G GAMMA-4 CHAIN C REGION.
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PROSITE; PS00290; IG_MHC; 2.
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SEQUENCE OF 1-30 AND 81-326,
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Prinary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-77118561; PubMed-402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Michaelsen T.E., Frangione C., Franklin E.C.;
Primary structure of the 'hinge' region of human 1gG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
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-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
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:ION (HEAVY CHAIN DISEASE PROTEIN) (HDC).
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                          INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                 INTERCHAIN (WITH A HEAVY CHAIN). INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                Length 327;
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MEDLINE-8224785; PubMed-6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy Chain disease in man: cDNA sequence supports gene deletion model.";
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Pred. No. 7.1e-72;
8; Mismatches 6; Indels
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MEDLINE-81021548; PubMed=6774747;
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21-JUL-1986 (Rel. 01, Last seq
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                                                                                        AMSCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CHI REGION.

MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.

MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAINS UBCLASS.

MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOOR TIMES AS LONG AS IN OTHER GAMMA CHAINS THE INDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
                                     MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN. MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; 1.
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MIM; 147120; -.
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DB 1; Length 290;

Score 1126;

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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-84030930; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Fd sections of rabbit
                                                              64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKWYVD 123
                                                                                                  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                                  122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                          Gaps
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                                                                                                                                                               184 GQPREPQVYILPPSREEMIKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTIPPMLDS
                                                 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last annotation update)
1G GAMMA CHAIN C REGION.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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Sequence studies of the Fd section of the heavy chain of
                          Indels
                                                                                                                                                                                                 182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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(In) Killander J. (eds.);
                                                                                                                                                                                                               244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK
Pred. No. 2.6e-71;
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                       13; Mismatches
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"Sequence studies on the constant region of immunoglobulin G of different allotype.";
Biochem. J. 151:337-49(1975).
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           90.38;
                        205; Conservative
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SEQUENCE OF 1-128.
           Best Local Similarity
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P01870;
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(See http://www.isb-sib.ch/announce/
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MEDILINE-11058411; Pubmed-5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TISKARGQPLEPKVYTMGPPREELSSRSVSLJCMINGFYPSDISVEWEKNGKAEDNYKTT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 PAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK
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REF. 2).
EF. 3 AND 4).
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-> S (IN REF. 5).
69E8AA118D579A8B CRC64;
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                                                                                                                                                                           D11 MARKER).
E15 MARKER).
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21.JUL-1986 (Rel. 01, Last sequence update)
12.JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2 CHAIN C REGION.
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Submitted (APR-1975) to the PIR data bank
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PROSITE; PS00290; IG_MHC; 1.
                                             EMBL; M16426; AAA31289.1;
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185
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323 AA;
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                                                               A02161; GHRB
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SEQUENCE OF 1-3.
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CH1.
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CH2.
CH3.
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Best Local Similarity 67.09
Matches 150; Conservative
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"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN PIR; A02151; G2GP.
                                                                                    pig
the carboxyl-terminal
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                                                                                                                                                                                                                                                      SEQUENCE OF 227-311.
MEDLINE-75036073; PubMed-4609467;
MISLINE-75036073; PubMed-7.3.;
"Primary structure of the CH3 homology region from guinea pig 1g62 antibodies.";
                                                                                                                                                                                  Tracey D.E., Cebra J.J.; "Primary structure of the CH2 homology region from guinea pig IgG2 antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN).
CHAIN).
CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain; Immunoglobulin C region; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.6%; Score 889; DB 1; Length 329; 72.3%; Pred. No. 7.5e-55; ive 24; Mismatches 36; Indels
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INTERCHAIN (WITH A HEAVY
INTERCHAIN (WITH A HEAVY
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36074 MW; 5D231B7164D1FBA9 CRC64;
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                                                                Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-(6/2). II. Amino acid sequence of and hinge region cyanogen bromide fragments."; Biochemistry 10:9-17(1971).
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC.
                                       SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                     MEDLINE-75036072; PubMed-4429665;
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                                                                                                                                                                                                                             Biochemistry 13:4796-4803(1974).
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PROSITE; PS00290; IG_MHC; 1.
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INTERPRO; IPR000495; ...
INTERPRO; IPR003006; ...
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79
105
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                                                                                                                                                         SEQUENCE OF 134-226.
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RESULT 7
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10.1-FEB-1991 (Rel. 17, Created)
10.1-FEB-1991 (Rel. 17, Last sequence update)
11.5-JUL-1999 (Rel. 18, Last sequence update)
11.5-JUL-1999 (Rel. 18, Last annotation update)
11.6 GAMMA-2B CHAIN C REGION.
11.6 GAMMA-2B CHAIN C REGION.
11.7 GAMMA-2B CHAIN C REGION.
12.8 GAMMA-2B CHAIN C REGION.
13.8 GAMMA-2B CHAIN C REGION.
14.8 GAMMA-2B CHAIN C REGION.
15.8 GAMMA-2B CHAIN C REGION.
16.8 GAMMA-2B CHAIN C REGION.
17.8 GAMMA-2B C REGION.
17.8 GAMMA-2B C REGION.
18.8 GAMMA-2B C R
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01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G GAWMA-3 CHAIN ERGION, SECRETED FORM.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-855027161; PubMed-6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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398 AA;
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                            Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                          Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene.";
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HEAVY CHAIN).
HEAVY CHAIN).
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                                                                                                                                    INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                    Length 333;
                                                                                                                                                                                                                                                   Score 838; DB 1; Length 33
Pred. No. 2.6e-51;
3; Mismatches 42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         186 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
                                                                                                                 Immunoglobulin domain; Immunoglobulin C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-84041483; PubMed=6314258;
Komaromy M., Clayton L., Rogers J., Robertson
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Nucleic Acids Res. 11:6775-6785(1983).
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       SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed-3149946;
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66.48;
                                                                                           PFAM; PF00047; 1g; 3.
PROSITE; PS00290; IG_MHC; 1.
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                                                                      INTERPRO; IPR000495; -.
                                                 Gene 74:473-482(1988).
PIR; PS0018; PS0018.
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PIR; PS0017; PS0017.
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Mämmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                             C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 398;
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-1 CHAIN C REGION.
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POTENTIAL.
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PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                              Alternative splicing.
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HINGE.
CH2.
                                                                                                                                           EMBL; J00451; AAB59655.1; -.
EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02155; G3MSM.
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INTERPRO; IPR003006; -.
PFAM; PF00047; 1g; 3.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE-80012837, PubMed-113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDILTRE-80202559; PubMed-6769752;
Obbita M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Takahashi I., Mano Y.;
Gericoning and complete nucleotide sequence of mouse immunoglobulin gamma l chain gene. ".
Cell 18:559-568(1979);
                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
013BAB45EF49B9DA CRC64;
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                                                               CHAIN).
CHAIN).
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Pred. No. 5.6e-50;
l; Mismatches 35;
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32-JUL-1986 (Rel. 01, Last sequence update)
30-MXY-2000 (Rel. 39, Last annotation update)
IG GAMMA-1 CHAIN C REGION.
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63.18;
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                                                                                                         DISULFIDE BONDS (MOPC 21).

MEDLINE=73008889; PubMed=5073237;

Svasti J., Milstein C.;

The disulphide bridges of a mouse immunoglobulin G1 protein.";

Biochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN).
CHAIN).
                                 "Evolution of immunoglobulin subclasses. Primary structure of murine myeloma gammal chain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing.
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; Pred. No. 6.6e-50;
44; Mismatches 35;
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HINGE.
                                                    ine myeloma gammaí chain.";
Biol. Chem. 253:6068-6075(1978)
MEDLINE=78242288; PubMed=98524;
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PROSITE; PS00290; IG_MHC;
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INTERPRO; IPR000495; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-44 FROM N.A.

MEDLINE=8222190; PubMed=6283537;
Yamawaki-Kateaka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kateaka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-1-ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES BUCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOWOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Clothing and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                        Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 323-366 FROM N.A.
MEDILINE=8115295; PubMed=6799207;
KROGETS J., Chol E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                          "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
                                              21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
                          393 AA.
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SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
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                        STANDARD;
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                                                                                                                                                                                                                                                                                              5;
                  LIGHT CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
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4CC88343B7A1CE27 CRC64;
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                                                                                                                                                                                                                                                      Query Match 36.2%; Score 812.5; DB 1
Best Local Similarity 62.3%; Pred. No. 1.8e-49;
Matches 139; Conservative 44; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2C CHAIN C REGION.
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PROSITE; PS00290; IG_MHC; 1.
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INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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Ollo R., Adfray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                       VHNĄKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
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Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
The complete nucleotide sequence of mouse immunoglobin gamma 2a gene "The complete nucleotide sequences of mouse immunoglobin jamma 2a gene and evolution of heavy chain genes: further evidence for intervening and evolution of heavy chain genes: further evidence for intervening
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"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-81076554; Pubmed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
Structure of the constant and 3' untranslated regions of the Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                     CHAIN).
CHAIN).
                                                                                                 DB 1; Length 329;
INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                       Indels
                                                                5FCD7B7933850773 CRC64;
                     (WITH A HEAVY (WITH A HEAVY
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                                                                                                Score 809.5; DB 1
Pred. No. 2.4e-49;
1; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
32-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
IG GAMMA-2A CHAIN C REGION, A ALLELE.
                                                                                                                                                                                                                                                                                                                                                      330 AA
                     INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; Pubmed=4831970;
                                                                                                                       41;
                                                                 MM;
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63.8%;
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329 AA;
                                                                                                           Similarity
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Matches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                      de Preval C., Fougereau M.; "Determination of the primary structure of a mouse gamma G2a "metermination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Biochem. 30:452-462(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMOVED POST-TRANSLATIONALLY.
B84361C5445A6864 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
MUS musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%; Score 809; DB 1;
65.2%; Pred. No. 2.6e-49;
ive 30; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain; Immunoglobulin C region.
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MEDLINE-73056887; PubMed-4565406;
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PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunog NON_TER 1 1
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nes 146; Conservative
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ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAÎN TWO MRNA SPECIES FOR IG GAMAA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMAA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED SEGMENT OF MU CHAINS. THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.

MISCELLANEOUS: THE SEOURNCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
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N-LINKED (GLCNAC. .) (POTENTIAL).
4C38138BFAED3FF0 CRC64;
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65.0%; Pred. No. 7.2e-49;
Live 30; Mismatches 46; Indels
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PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 65.09
Matches 145; Conservative
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INTERPRO; IPR000495; -.
INTERPRO; IPR003006; -.
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287 YFWYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329 185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227 g ŏ

107 CPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE 166

7 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 64

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Gaps

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125 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPPVLDSDGS 184

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OM protein - protein search, using sw model

March 1, 2001, 09:15:49 ; Search time 79.26 Seconds Run on:

(without alignments)
343.530 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-389-782A-8 2246 1 MDKTHTCPPCPAPELLGGPS.....QKGNATHDNICSGNSESTQK 401

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 Total number of hits satisfying chosen parameters:

195891 segs, 67,900655 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_66:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Ig gamma-1 chain C		heavy cl	ь	g gamma chain C		g gamma-3 chain	5	g gamma-4 chain	g gamma-	g gamma ch	g gamma	Ig gamma 2a chain	5	5	Б	6	6	g heavy chain		5	6	ь	_	Ig gamma-1 chain C	g gamma-1 chain	g gamma-1 chain	gamma-2c	6
ΩI	831866	GHHD	869339	S72664	PT0207	A23511	A60764	GZHU	G4 HU	G3HUWI	GHRB	147160	147159	147162	GZGP	I47158	147161	\$22080	C30554	<b>S31459</b>	G3MSC	PS0018	G3MSM	PC4436	PS0017	GIMS	G1MSM	S00847	G2MSA
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Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2 chain C	Ig gamma'-2b chain	Ig gamma heavy cha	Iq heavy chain VHI	Ig heavy chain V-I	Ig gamma-1 chain C	Ig Y heavy chain (	Ig mu chain C regi
S37483	G2MSAM	G2MSAB	S40295	PS0019	G2MS11	S25057	G2MSBM	S06611	S01321 ·	146732	S69340	A36040	S14236	B46529	S25644
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469	399	332	446	322	336	474	405	327	475	180	249	218	152	572	343
36.0	35.8	35.7	35.4	35.0	34.7	34.7	34.5	34.0	33.7	31.5	25.7	25.6	25.4	17.6	16.1
809	804	802	794	785.5	779	779	774	764	757	707	577.5	574.5	571	395.5	362
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1 S31866 Ig gamma-1 chain C region - synthetic C:Species: synthetic A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000 C;Accession: S31866 R;Filpula, D. S:Monitted to the EMBL Data Library, February 1993
· .	A; Description: Screeing method for protein-protein interactions of cloned gene produc A; Reference number: \$31866 A; Reference number: \$31866 A; Molecule type: mRNA A; Residues: 1-255 <fild. ,="" 1-22="" 1-255="" 23-255="" 933068;="" 933069="" <fild.="" a="" a;="" bscherichia="" c="" c;="" caa49866.1;="" chain="" coli="" cross-references:="" embl:="" f;="" gamma-1="" human="" ig="" immunoglobulin="" membrane="" nid:="" outer="" pid:="" pidn:="" precursor="" protein="" region:="" region<="" residues:="" reywords:="" td="" x70421;=""></fild.>
•	Ouery Match 54.9%; Score 1233; DB 4; Length 255; Best Local Similarity 100.0%; Pred. No. 9.6e-72; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy 2 DKTHTCPPCPAPELLGGPSVFLFPPKRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
	QY 62 GVEVHNAKTRPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAK 121 
	Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181

Matc	Matches	227;	Cons	227; Conservative			0; Mismatches	ches	0; Indels	Inc	le1s	0;	Gaps	Ø
Qy	.~	DKTHTC	PPCPA	2 DKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61	VFLFP	PKPI	KDTLMI	SRTPEVI	CVVVI	OVSE	EDPEVK	NWYV	Θ-	н
q	29	DKTHTC	PPCPA	DKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	VFLFP	PKPI	KDTLMI	SRTPEVI	CVVI	OVSE	EDPEVKI	FNWYV	D 88	8
ΟŊ	62	GVEVHN	AKTKE	62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAK 121	YRWS	VLT	VLHQDW	TURKEYR	CKVS	NKAL	PAPIEK	FISKA	× -	21
qq	89	GVEVHN	AKTKF	89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148	YRVVS	- Z-	VLHQDW	ALNGKEYR	CKVS	NKAL	PAPIEK	LISKA	í ж-	48
Οy	122	GOPREP	DVYTE	122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181	KNOVS	LTC	LVKGFY	PSDIAVE	SWESNO	SOPE	NNYKTTI	PPVLD	S	81
Db	149	GQPREP	OVYTI	GQPREPQVTILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 208	KNQVS:	LTC]	LVKGFY	PSDIAVE	MESNO	SOPE	NNYKTT	PPVLD		80
δy	182	DGSFFL	YSKLI	182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228	GNVFS	CSVI	MHEALE	INHYTOKS	STSTS	PGK	228			
qq	209		XSKLI	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255	GNVFS	CSVI	MHEALE	INHYTORE	STSTS	PGK	255			

## RESULT

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Gaps 61

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Gaps

ó 374;

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin c region; immunoglobulin homology (S; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM3> F;27-85/Domain: immunoglobulin homology <IM3> F;24-310/Domain: immunoglobulin homology <IM3> F;27-310/Domain: immunoglobulin homology <IM3> F;27-83,144-204,250-308/Disulfide bonds: #status experimental F;109,112/Disulfide bonds: interchain (to light chain) #status experimental F;109,112/Disulfide bonds: interchain (co light chain) #status experimental F;109,112/Disulfide bonds: interchain (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C: Species: Homo sapiens (man)
C: Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C: Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C: Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000
C: Accession: S69339
R: Khamlichi, A.A.: Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A: Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A: Recession: S69339
A: Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A: Accession: S69339
A: Status: preliminary
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Residues: 1-374 < K HA>
A: Cross-references: EMBL: X81695
C: Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DKTHICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.9%; Score 1233; DB 1;
100.0%; Pred. No. 1.3e-71;
ive 0; Mismatches 0;
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Pred. No. 3.5e-71;
2; Mismatches 0;
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illarity 99.1%;
Conservative
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Best Local Similarity 100.
Matches 227; Conservative
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Best Local Similarity
Matches 225; Conserv
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A; Contents: myeloma protein Nie
A; Reference number: A91668; MUID:77070269
A; Contents: myeloma protein Nie
A; Contents: myeloma protein Nie
A; Contents: myeloma protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, (0',36-96, 'K',98-115, 'Q',117-197, 'D',199-238,'D',240,'L',242-268,'E',27
A; Note: this sequence has the Gin(17) and Gin(1) markers
R; Schmidt, W.E.; Uung, B.D.; Palm, W; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Reference number: A91723; MUID:83289131
A; Reference number: A91723; MUID:83289131
A; Molecule type: protein
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A; Reference number: A90565; MUID:71064027
A; Contents: annotation: disulfide bonds
B; Dreker, L.: Schwarz, J.: Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure: The primary structure of monoclonal IgG1 immunoglob
A; Reference number: A91667; MUID:77070267
A; Contents: annotation; disulfide bonds
A; Reference number: A91667; MUID:77070267
A; Contents: annotation; disulfide bonds
A; Reference number: A91667; MUID:77070267
A; Contents: annotation; disulfide bonds
A; Reference number: A91667; MUID:77070267
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A; Residues: 88-113;235-330 <TAK>
A; Residues: 88-113;235-330 <TAK>
A; Cross-references: EWBL:21730,
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequent
A; Reference number: A90563; MUID:71064024
A; Contents: myeloma protein Eu
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A; Residues: 1-96, TR', 98-135 <CUN>
A; Note: Its sequence has the Glm(3) marker, 97-Arg
A; Note: Luningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque
A; Reference number: A90564; MUID:71064025
A; Contents: Eu
A; Accession: A90564
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A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
                                                                                                         A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A;Note: Lys-330 is removed after translation
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A; Residues: 2-330 < RAR>
A; Residues: 2-330 < RAR>
A; Residues: 2-330 < RAR>
A; Cross-references: EMBL: 217370
B; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of A; Reference number: S33887; MUID:83001943
A; Accession: S33887
                                                                                                                                                                                                                         Library, October 1992
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A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
                                                                              A; Cross-references: EMBL: Z17370
                                                                                                                                                                                                              A; Reference number: S33904
A; Accession: S36861
A; Molowile
                                                                                                                                                                                        R; Harris, L.J.
submitted to the EMBL
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Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1227; DB 2;
Pred. No. 3.5e-71;
2; Mismatches 0;
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                                                                                                                                                             submitted to the EMBL Data Library, September 1994 A. Reference number: S72664 A. Accession: S72664 A. Status: preliminary
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ilarity 99.1%;
Conservative
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Best Local Similarity 98.6
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-374 <KHA>
                                                                                                 C; Accession: S72664
R; Khamlichi, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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an IGHG4 conv
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R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                      Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 14-May 1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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A; Map position: 14q32.33-14q32.33
A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-377 <HUC>
C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin C; Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c3,
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Score 1146; DB 2;
Pred. No. 5.1e-66;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Gmb0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.16
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A60764
R;Huck, S.; Lefranc, G; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele
A;Reference number: A60764; MUID:90007613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma-3 chain C region, form LAT - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.0%;
92.5%;
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Matches 210; Conserv
                                                                                                                                                                                                                                                                                                                                 1-377 <HUC>
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                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                            A; Accession: A235
                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: IGHG3
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                   195
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Gaps

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Length 377;

Score 1144; DB 2; Pred. No. 6.8e-66; 8; Mismatches 9;

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Matches 210; Conservative Similarity

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Query Match Best Local 3

50.9%; 92.5%;

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61

us-09-389-782a-8.rpr

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A; Notecella type: DNA
A; Residues: 1-327 < ELL>
A; Note: the Sequence was determined from the germline gene
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: human immunoglobulin sublclasses. Partial amino acid sequence of the constan A; Reference number: A90249; MUID:70207560
A; Molecule type: protein
A; Residues: 1-30; 81-326 < PIN>
C; Genetics: A; Genetics: C C Genetics: A; Genetics: BDB:119340; OMIM:147130
A; Map position: 14432.33-14432.33
A; Thtrons: 9947; 111/1; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical into disulfide bonds. In some cases, such as IgA and IgM, the subunits associat into C; Superfamily: immunoglobulin hemology < IMD>
C; Superfamily: immunoglobulin homology < IMD>
F; 20-85/Domain: immunoglobulin homology < IMD>
F; 20-107/Domain: immunoglobulin homology < IMD>
F; 20-107/Domain: immunoglobulin homology < IMD>
F; 240-307/Domain: immunoglobulin homology < IMD>
F; 240-307/
                                                            A, Coss. references: GDB:119338; OMIM:147110
A; Cross-references: GDB:119338; OMIM:147110
A; Cross-references: GDB:119338; OMIM:147110
A; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
C; Complex: An immunoglobulin c region; immunoglobulin homology when immunoglobulin c region; immunoglobulin homology cost c Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 20-85/Domain: immunoglobulin homology cim2>
F; 133-202/Domain: immunoglobulin homology cim2>
F; 133-202/Domain: immunoglobulin homology cim2>
F; 134-140-200, 246-304/Disulfide bonds: #status experimental
F; 27-83,140-200, 246-304/Disulfide bonds: #status experimental
F; 102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Caccession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFF 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 326;
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Pred. No. 7.2e-66;
8; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.9%;
larity 94.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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A; Mesidues: 1-24, E' 26-57, EV', 60-85,132-171, 'ZZZ', 175,'B',177-193,'D',195-196,'Q',198-A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
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A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
KWang, A.C.; Tung, E.; Evdenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A;Reference number: A92809; MIID:81007873
A;Accession: A92809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin A;Reference number: A93132; MUID:80114419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Coinell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of
A; Reference number: A90752; MUID:80001357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C'Species: Homo sapiens (man)
C'Date: 30-Apr-1081 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and Sequence homology of two human immunoglobulin gamma heavy chain A;Reference number: A93906; MUID:82197621
122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Reference number: A90235; MUID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
                                                                                                                    GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-2 chain C region - human
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A; Accession: A90752
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17-225, 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Milstein, C.; Frangione,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-326 <ELL>
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C; Comment: The heavy chain disease protein Wis
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on. Residue 12 co
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A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quadruplication
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A; Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A; Reference number: A93915; MUID:82247835
A; Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Accession: A9042

A Molecule type: protein

A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain

A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 or

A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 or

A; Note: the sequence of residues 42-76 was taken from the reference that follows

R; Michaelsen, T.E.; Frangione, B; Franklin, B.C.

A; Biol. Chem. 252, 883-889, 1977

A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication

A; Reference number: A92219; MUID: 7718861

A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inters. KNolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A;Keference number: A90198; MUID:77021516
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues A;Accession: A90198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy
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A; Residues: 12-97 <MIC>
A; Note: the hinge region in gamma-3 chains is about four times as long as in other
idue segment (12-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C. Accession: A90442; A92219; A90188; A93915; A02149
B. Frandione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Blochemistry 19, 4304-4308, 1980
A. Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 A. Reference number: A90442; MUID:81021548
A. Contents: heavy chain disease protein Wis
                                                                                                                                                                                                                                    ö
                                        experimental
                                                                                                                                                                                                                                                                                          PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                    ö
F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status exper F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                Length 327;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1135; DB 1;
Pred. No. 2.2e-65;
8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma-3 heavy chain disease proteins - human
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A; Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
                                                                                                                                                                Query Match 50.5%;
Best Local Similarity 93.7%;
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A92219
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A. Accession: A9020: MOLE: O. 1939409
A. Accession: A9030: MOLE: O. 1939409
A. Accession: A9030: Mole: D. 1982
A. Residues: 1-47, E', 49-71, PV', 72-128 CPRA>
B. Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S. 79, 6018-6022, 1982
A. Title: Heavy chain genes of rabbit 19G; isolation of a cDNA encoding gamma heavy chain genes of rabbit 19G; isolation of a cDNA encoding gamma heavy chain genes of rabbit 19G; isolation of a cDNA encoding gamma heavy chain genes of the 13399917
A. Accession: A9328
A. Molecule type: mRNA
A. Accession: A9328
A. Molecule type: MIND: 19165111; PIDN: AAA31289-1; PID: 9165112
A. Mote: this sequence has the dl1 allotypic marker, 104-Met, and the essant R. Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
B. Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
B. Fruchter, R.G.; Sequence studies of the Rd section of the heavy chain of rabbit immunoglobul A. Reference number: A90245; MUID: 70110015
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A;Residues: 132-143, E', 145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wikse
A;Reference number: A94416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 DIPPPCPRCPAPELLGGPSVFLFPPKPKDILMISRIPEVICVVDVSHEDPEVQFKWYVD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 243
C;Genetics:
A;Gene: OBB:1GHG3
A;Cross_references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid C;Reywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid C;Reywords: duplication; glycoprotein; immunoglobulin homology xIMM.
F;203-270/Domahn: immunoglobulin homology xIMM.
F;1/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change G
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change G
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, KE.; Alaxander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the A;Reference number: A91749; MuID:84030330
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        marker, 104-Thr, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 49.9%; Score 1121; DB 1;
Best Local Similarity 90.3%; Pred. No. 1.5e-64;
Matches 204; Conservative 13; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region of
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A; Residues: 1-323 GBEA
A; Note: this sequence has the d12 allotypic: 1
R; Pratt, D.M.; Mole, L.E.
Biochem, J. 151, 337-349, 1975
A; Title: Sequence studies on the constant re-
A; Reference number: A90290; MUID:76135469
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328

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5

Gaps

., m

Indels

28;

Length 328

DB 2;

224

the cDNA sequences

A; Accession: A94416

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19 jamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence
A;Reference number: 147158; MUID:95015845
A;Accession: 147159
A;Accession: 147159
A;Accession: 147159
A;Accession: 147159
A;Accession: 147159
A;Residues: 1-328 «KAC>
A;Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C;Genetics:
A;Gene: IgGsa
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gigadima 4 chain constant region - pig (fragment)
Cispecies: Sus scrofa domestic pig)
Cispecies: Sus scrofa domestic pig)
Cispecies: Sus scrofa domestic pig)
Cispecies: 11-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
Ciscession: 147162
Ricacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the CDNA sequence number: 147158; MUID:95015845
A:Reference number: 147158; MUID:95015845
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 YFLYSKFSVDKASWQGGSIFQCAVMHEALHNHYTQKSISKTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.2%; Score 903.5; DB 2 ilarity 71.1%; Pred. No. 9.9e-51; Conservative 30; Mismatches 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.4%; Score 906.5; DB 2
Best Local Similarity 73.2%; Pred. No. 7.6e-51;
Matches 164; Conservative 29; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                          A; Wolecule type: protein
A; Rosidues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'O',
A; Rosidues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'O',
A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into la
C; Superfamily: immunoglobulin cregion; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
E; 20-82, Domain: immunoglobulin homology < IM1>
F; 30-92, Domain: immunoglobulin homology < IM2>
F; 303, Domain: immunoglobulin homology < IM3>
F; 3180-199, Domain: immunoglobulin homology < IM3>
F; 318-199 H; Minoglobulin homology < IM3>
F; 318-199 H; Minoglobulin homology < IM3>
F; 318-199 H; Minoglobulin homology < IM3>
F; 173, Minog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequences of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
R; Racskovics, I:; Sun, J:; Butler, J.E.
J. Immunol. 153, 3563-3573, 1994
A; Title: Five putative subclasses of swine IgG identified from the cDNA sequa A; Reference number: I47158; MUID:95018845
A; Accession: I47160
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: I-328 < KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 323;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.9%; Score 918.5; DB 1
71.7%; Pred. No. 1.3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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Matches 164;
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4

Gaps

Indels

31; DB 2;

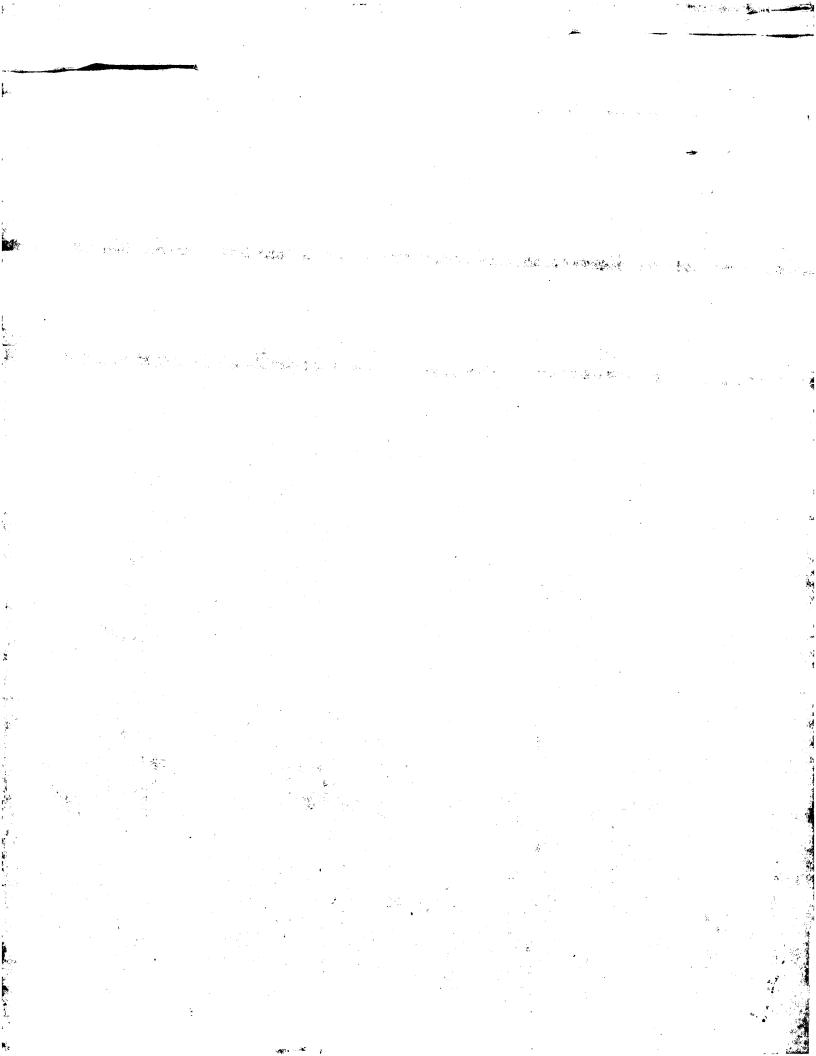
Length 277;

the cDNA sequences

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Search completed: March 1, 2001, 09:15:50 Job time: 148 sec
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A;71tle: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474
A;Reference number: A90354; MUID:71058474
A;Rotents: annotation; disulfide bonds
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap and igal) and igal, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keyvords: duplication; glycoprotein; heterotetramer; immunoglobulin
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MUID:71058486
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A;Residues: 134-226 <TRA>
R;Triscimann, T.M.; Cebra, J.J.
R;Chenistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MuID:75036073
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Blochemistry 13, 4796-4803, 1574
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. A;Reference number: A90352; MUID:71058471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
                                                          56 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 115
                                                                                                    103 FSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITR 162
                                                                                                                                                                                                                                 43 VDKRVGTKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQ 102
                                                                                                                                                                                                  116 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYK 173
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F:241-310/Domain: immunoglobulin homology <IM3>
F:26-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                        174 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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submitted to the Atlas, April 1975
A;Reference number: A94553
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A; Residues: 69-133;312-329 <TUR>
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A; Residues: 4-68 (BIR>
R; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy ci
A; Reference number: A90359; M
A; Accession: A90359; M
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A; Residues: 227-311 <TR2>
R;Oliveira, B.; Lamm, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-3 <TRI>
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66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
                                                                                                                  65
                                                                                    Gaps
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                                                                                                                                                                                                                                               126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG
                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                  184 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                  1;
                                                  ; DB 1;
1e-49;
                                                                                 24; Mismatches
F;248-308/Disulfide bonds: #status experimental
                                                  Score 889;
Pred. No. 1
                                                39.6%;
ilarity 72.3%;
Conservative 2
                                                Query Match
Best Local Similarity
Matches 162; Conserv
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

March 1, 2001, 09:17:08; Search time 70.93 Seconds Run on:

(without alignments) 193.313 Million cell updates/sec

US-09-389-782A-8

Perfect score:

1 MDKTHTCPPCPAPELLGGPS.....QKGNATHDNICSGNSESTQK 401 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

268485 seqs, 34193795 residues Searched:

268485 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

| SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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| SIDSI/gcgdata/geneseqp/AA1986.DAT:*
| SIDSI/gcgdata/geneseqp/AA1986.DAT:*
| SIDSI/gcgdata/geneseqp/geneseqp/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:* /SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT: /SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Heavy chain of hmA	Recombinant human	Recombinant human	Amino acid sequenc	Chimeric receptor	Chimeric receptor	CD2 binding LFA-3-	Human transmembran	Rabbit TGFbetaRII:	Human TGFbetaRII:F	Amino acid sequenc	Amino acid sequenc
	ΩI	W48650	W83963	W49075	X01372	W26649	W26650	R27163	Y83136	W73513	W73514	Y54063	Y54064
	DB	19	19	19	20	18	18	13	21	19	19	21	21
	Query Match Length DB	652	374	374	235	651	692	347	347	388	388	388	388
dP .	Query Match	55.2	55.1	55.1	55.1	55.1	55.1	54.9	54.9	54.9	54.9	54.9	54.9
	Score	1239.5	1238	1238	1237	1236.5	1236.5	1234	1234	1234	1234	1234	1234
•	Result No.	н	8	e	4	S	9	7	80	6	10	11	12

Human interferon-b	Human interferon-b	Human interferon-b	VCAM 2D-Igg. Homo	VCAM 2D-IgG, a sol		A VCAM 2D-IqG1 fus	Human cytokine rec	Human IgG1 hinge/F	Human Fc (19G1).	Protein from pCd51	Human immunoglobul	Human kappa immuno	Sequence of the li	Linkered human IgG	Antigenic peptide	ţ	Recombinant human	Recombinant human	IL4.Y124D/IgGl pro	Aggrecanase artifi	ar		Human soluble kit	Human soluble kit	ce of c		+-		Q	Human IgG1 chain C	Completely humanis	Amino acid sequenc
X70867	Y70868	X70869	R58753	Y23986	Y01037	W96743	W31646	W26232	X06617	Y24154	R91806	R43685	P91918	P93558	W60037	W83962	W49073	W49074	R90920	W18574	W18575	Y15123	W14764	W14765	R26530	W10552	W10550	Y24153	582	X31669	R43339	W49816
21	21	21	12	20	20	20	19	18	20	20	17	14	10	10	19	19	19	19	17	18	18	21	16	16	13	18	18	20	17	20	14	19
399	418	423	446	446	446	446	482	232	233	259	329	351	371	371	376	379	379	379	387	396	366	400	424	424	435	437	442	4	446	447	449	449
	54.9			٠.			٠.	•	٠.	54.9	•		54.9	٠.		•	54.9	54.9		٠.		54.9			٠						٠	
(2)	1234	3	3	3	3	3	m	3	3	m	3	23	23	23	23	3	23	23	1233	23	23	3	3	3	3	n	3	3	3	3	3	3
13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	. 37	38	33	40	41	42	43	44	45

## ALIGNMENTS

W48650 standard; Protein; 652 AA. (first entry) 04-AUG-1998 W48650; RESULT W48650

Heavy chain of hmAb425 fused to TNF alpha.

Antibody-cytokine fusion protein; tricistronic vector; chimeric; TNF alpha; IL-2; IRES; internal ribosome entry site. 

Synthetic

Homo sapiens

1...tote="Heavy chain of human mAb 425" 495..652 /note= "INF alpha" Location/Qualifiers 1..494 Key Region Region

WO9811241-A1

19-MAR-1998.

97WO-EP04765 02-SEP-1997; 96EP-0115635. 96EP-0114820. 30-SEP-1996; 16-SEP-1996; (MERE ) MERCK PATENT GMBH.

Hauser H, Mielke C; Bruemmer W, Burge C, Dunker R, Rieke E, Von Hoegen I, Welge T; Homo sapiens.

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9
                                                                                                                                               The present sequence represents a fusion protein comprising of TNF alpha fused to the C-terminus of the heavy chain of the human monoclonal antibody 425 (hmb425). The hmb425 has specificity for the human EGF receptor. The invention claims for a new pMCLDHAP tricistronic vector (V18096) for the expression of an antibody-cytokine tusion protein, hmb425-TNF alpha. The TNF alpha sequence can be substituted by the IL-2 sequence. The vector also contains a strong promoter/enhancer unit, a selection marker gene and at least two poliovirus derived internal ribosomal entry site (IRES) sequences. The vector can be expressed in mammallan host cells for the production of heteromeric fusion proteins. This expression system is claimed to produce the heteromeric proteins in high yields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPKYLHYDEE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCK-ELQYV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | | | | 525 nrranallangvelrdnglvvpseglyliysqvlfkgggc-psthvllthtisriavsyg 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 KQECNR-----THNRVCECKEGRYL-EIEFCLKHRSCPPGFGVVQAGTPERNTVCKR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVŢCVVVDVSHEDPEVKFNWYVD 61
                                                                 Oligo:cistronic expression vector - useful for production of, e.g. MAb425/TNF-^a or MAb425/IL-2 antibody fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB; obesity; human; adiposity; blood lipid; diabetes type II; insulin; hypoglycaemic; antihypertensive; diuretic; appetite suppressant; suspension; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1239.5; DB 19; Lengt; Pred. No. 9.4e-76; 19; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant human metFc-OB protein variant.
                                                                                                                 Disclosure; Fig 15; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                             55.2%;
65.8%;
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584 tkvnlls---aikspcgret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 CPDGFFSNETSSKAPCRKHT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 65.89
50; Conservative
              1998-207400/18
                                                                                                                                                                                                                                                                                                                                                                             652 AA;
                               V18096
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Best Local Simil
Matches 250; C
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                               N-PSDB;
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This represents a recombinant metFc-OB protein variant which consists of an FC region of human immunoglobulin (19) fused to a human OB (obesity) protein. The invention provides a human OB protein suspension that contains at least 0.5 mg/ml of the human OB protein derivatised by attachment of the FC region of an Ig to the N-terminus of OB, and has a pH 6-8. The suspensions are used to reduce weight, adiposity and blood lipid levels, to treat or prevent diabetes type II, and to increase lean mass and insulin sensitivity. They may be used in conjunction with insulin, hypoglycaemics, antihypertensives, diuretics, appetite suppressants etc. These suspensions are stable and active at physiological pH and are ready-for-use formulations that do not require freezing or freezed drying. As they are very concentrated, only small volumes are required and they provide a sustained-release effect, with increased potency and reduced frequency of injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Concentrated suspension of fusion of obesity protein with Fc immunoglobulin fragment - stable at physiological pH, used for erreduction of weight and blood lipid levels, and for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPGK 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1238; DB 19;
Pred. No. 6.1e-76;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.1%; Scc...
100.0%; Pre/
0; N
                                                                                                                                                                                                                                                                                                                                                 2; Fig 6A-C; 47pp; English.
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                                                                                                                                                                                              Speed MA
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                                                                                                                   98US-0059467
                                                                                       98WO-US07828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                              French DL,
                                                                                                                                                                                                                            1998-594525/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 AA;
                                                                                                                                                                                                                                                                                                                type II diabetes
                                                                                                                                                                                                                                          N-PSDB; V69686
                             WO9846257-A1.
                                                                                       16-APR-1998;
                                                                                                                     14-APR-1998;
17-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 228;
                                                           22-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1998
                                                                                                                                                                                              Brems DN,
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W49075
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Recombinant human MetFc-OB variant 2 protein.

pathogen; autoimmune disease; allergen; tumour; therapeutic; cytokine; chemotherapy agent; interferon; insulin; human growth hormone; fertility; drug; calcitonon; steroid; immunity; mucosal; AIDS; hepatitis; Fc; human; immunoglobulin; IgG.

/note= "encoded by TGA"

WO9904813-A1

04-FEB-1999.

. Misc-difference 230

Homo sapiens

FcRn; binding; epithelial cell; immune system; modulation; antigen;

Amino acid sequence of Fc fragment of human IgG.

(first entry)

04-JUN-1999

X01372;

Y01372 ID Y01372 standard; Protein; 235 AA.

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The present sequence represents a recombinant human MetFc-OB variant 2 fusion protein having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB protein sequence shown in w49073. The invention provides Fc-OB fusion proteins whereby the Fc region of an immunoplobulin or its analogue is linked, either directly or indirectly using a linker, to the N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins are claimed to demonstrate increased stability and clearance rate and decreased degradation as compared to OB protein or a fusion of Fc to the C-terminus of the OB protein. These Fc-OB fusion proteins are also claimed to be useful for treating excess weight in an individual or animal or for treating co-morbidities associated with excess fat such as diabetes, high blood lipid level, arterial sclerosis and stroke.
               Recombinant human MetFc-OB variant 2 protein; chimeric; immunoglobulin; high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
                                                                                                                                                                "Recombinant human Fc-OB variant 2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion proteins of OB and Fc - used for treating e.g. excess weight, diabetes, arterial sclerosis, arterial plaque, high blood lipid level, gall stones or stroke
                                                                                                                                                2.374 / note= "Recombinant human 229.374 / note= "Human OB protein"
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 5A-5C; 107pp; English.
                                                                                                                                                                                                                                                                                                     97WO-US23183
                                                                                                                                                                                                                                                                                                                                   96US-0770973
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-377658/32.
                                                                                                                                                                                                                                                                                                                                                                                                     Mann MB;
                                                                                                                                                                                                                                                                                                                                                                    AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 AA;
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                                                                                 Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                   10-DEC-1996;
                                                                                                                                                                                                                                  W09828427-A1
                                                                                                                                                                                                                                                                   02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                   Hecht RI,
                                                  diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                  Protein
                                                                                                                                                                                   Region
                                                                                                                                    Key
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The invention relates to methods of delivering molecules to a mammal by administering a conjugative of a therapeutic or a bloactive substance, and an FCRN binding partner targeted to epithelial cells expressing FCRN. This can be used for modulating a mammalian immune system wherein, the bloactive substance is an antigen characteristic of a pathogen of an autoimmune disease, an allergen, or a tumour. The delivering method is used to deliver therapeutics, including chemotherapy agents, cytokines including interferon, hormones, including insulin and human growth hormone, fertility drugs, calcitonon, calcitriol and other bloactive steriols to intestinal, murosal and lung epithelium. The method is also used for transepithelial delivery of antigens to provoke tolerance and immunity. The method provides an immunisation that specifically targets the mucosal surfaces, and does not have the risks associated with injections, including needle transmission of AIDS or hepatitis, of prior art immunisation methods. The present sequence represents the amino acid sequence of an Fc fragment of human immunoglobulin 19G.
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Pred. No. 4.1e-76;
2; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.18;
97.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.4
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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Gaps

Indels

Score 1238; DB 19; Pred. No. 6.1e-76; 0; Mismatches 0;

55.1%; bcc. 100.0%; Pre

Conservative

228;

Similarity

Query Match Best Local S: Matches 228

Length 374;

SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

181 181

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RESULT

dgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiska 120 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

61

g δy 셤

DGVEVHNAKTKPPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Delivering therapeutics, particularly antigens to epithelial cells comprises use of a conjugate of the therapeutic and an FCRn binding

Simister NE;

Lencer WI,

Blumgerg RS,

WPI; 1999-153297/13.

N-PSDB; X27800.

(BGHM ) BRIGHAM & WOMENS HOSPITAL. (UYBR-) UNIV BRANDEIS.

98WO-US15395 97us-0899856,

24-JUL-1998; 24-JUL-1997; 6

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This protein comprises a chimeric receptor consisting of an scrvengineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer comprising the human 1gG1 hinge. CH2 and CH3, linked to transmembrane and intracellular regions of the human T cell receptor zeta chain. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (See T90512) constructed from DNA cassettes encoding ach receptor component. In a claimed encoding a chimeric receptor containing 2 or more different cytoplasmic signalling components. Also claimed is use of DNA encoding a recombinant chimeric receptor in a DNA delivery system. The DNA delivery systems can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytolytic activity, differentiation or other effector functions, antibody secretion. They can be used in the treatment of e.g. increased adhesion. They can be used in the treatment of e.g. increased adhesion. They can be used in the treatment of e.g. increased adhesion. They can be used in the treatment of e.g. infectious disease, inflammatory disease, cancer, allergic/atopic disease, transplants and metabolic/idiopathic disease, claimed).
dgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiska 121
                                                                     181
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                                  IgG1: T cell receptor zeta chain; cell proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion, infection; cancer; allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes; graft versus host disease; human; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                  chimeric receptor; DNA delivery; CTMO1; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for activating cells - comprising DNA coding or comprising 2 or more different cytoplasmic
                                                                                                      SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weir ANC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawson ADG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CLLT ) CELLTECH THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                Chimeric receptor hCTMO1/G1/zeta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 7; 90pp; English.
                                                                                                                                                                                                                              651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB03209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bebbington CR, Finney HM,
                                                                                                                                                                                                                          W26649 standard; Protein;
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signalling components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-351052/32.
                                                                                                                                                                                                                                                                                                                                                                  activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T90512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9723613-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1996;
                                                                                                                                                                                                                                                                                              12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                                                                                            W26649;
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 62
                                                                                                                                      182
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                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                       61
                                                                                                                                                                             Gaps
In particular, they can be used in the treatment of rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, asthma, eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple sclerosis, organ or tissue transplant rejection, graft-versus-host disease or diabetes (claimed).
                                                                                                                                                                                                                                                                GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                           348 gvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskak
                                                                                                                                                                                                    2 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                        GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                    408 gqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppvlds
                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVK
                                                                                                                                                                                                                                                                                                                                                                                  DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPKYLHYDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 vkfsrsadapayqqqqqqlyn---elnlgrreeydvldkrrgrdpemg----gkprr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; 19G1; CD28; T cell receptor zeta chain; proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection: cancer; allergy; rheumatorid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes;
                                                                                                                                             Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQ 400
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                                                                                                                                             DB 18;
                                                                                                                                                                          61;
                                                                                                                                            55.1%; Score 1236.5; DB 62.6%; Pred. No. 1.5e-75;
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft versus host disease; human; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric receptor hCTMO1/G1/zeta-CD28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CLLT ) CELLTECH THERAPEUTICS LTD.
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                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                            Conservative
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                                                                                                                                                             Similarity
                                                                                                    AA;
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                                                                                                                                                                          258;
                                                                                                    Seguence
                                                                                                                                               Query Match
                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W26650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                          Matches
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R27163 standard; Protein; 347 AA.

RESULT R27163 (first entry)

20-MAY-1998

R27163;

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                                                                                                                                                                                                                                                    and CH3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKETFPPKYLHYDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ylldgilfiygviltalflr
                                                                                             New DNA systems for activating cells - comprising DNA coding for chimeric receptor comprising 2 or more different cytoplasmic
                                                                                                                                                                                                          This protein comprises a chimeric receptor consisting of an scFv engineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer comprising the Human 1gG1 hinge, CH2 and CH: linked to the transmembrane and intracellular components of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Length 692;
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Weir ANC;
Lawson ADG,
                                                                                                                                                                         8; 90pp; English.
Finney HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.68
Matches 258; Conservative
                                                                                                                                 signalling components
                                WPI; 1997-351052/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             692 AA;
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                                                                                                                                                                     Disclosure; Fig
Bebbington CR,
                                                    T90513
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                                                      N-PSDB;
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Gaps
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                                                                      lymphocyte associated antigen-3; T-lymphocyte accessory molecule; deletion mutant; CD2 binding site; immunomodulator; immunoglobulin; preLFA3TIP; LFA-3(92)1gG; pSAB152; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD2-binding domain of lymphocyte function associated antigen-3 and DNA - for diagnosing and treating inflammation and auto:immune diseases, e.g. systemic lupus erythematosus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
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Pred. No. 1e-75;
1; Mismatches
                                                                                                                                                                                  29.120
/label= LFA-3_aminoacids_1-92
                                                                                                                                                           1..28
/label= LFA-3_signal
                                              CD2 binding LFA-3-Ig fusion protein.
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                       /label= IgG1_hinge
131..239
                                                                                                                                                                                                                                               /label= IgG1_CH2
240..347
                                                                                                                                                                                                                                                                         /label= IqG1_CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Fig 12; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller GT, Rosa MD, Wallner·BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.9%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                    92EP-0104320.
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                                                                                                                                                                                                            121..130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in immunomodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-309760/38.
                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q28684
                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                       07-0CT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 227;
                                                                                                                                                                                                                                                                                                  EP503648-A.
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                                                                                                                                                                                      region
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MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

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Length 347;

DB 21;

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Selective modulation of memory effector T lymphocytes by administration of a CD2 binding agent which inhibits the CD2/LFA-3 interaction useful for treating conditions such as inflammatory bowel diseases, psoriatic
                                                              KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                                                          120 vdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyv 179
                                                                                                                                                                                                                                                                            memory effector T lymphocyte; psoriatic arthritis;
rheumatoid arthritis; multiple sclerosis; atopic dermatitis;
uveitis; inflammatory bowel disease; Crohn's disease;
ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulation of LFA3/CD2 interaction by administration of a CD2 binding
                     LFA3; CD2; cell signalling; modulation; lymphocyte; T cell; memory effector T lymphocyte; psoriatic arthritis;
                                                                                                        Human transmembrane LFA-3/IgG fusion protein LFA3TIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-76; 76pp; English.
                                                                                                                                                                                  AA.
                                                                                                                                                                                Y83136 standard; Protein; 347
                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0098456
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US20026
                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOJ ) BIOGEN INC
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                                                                                                                                                                                                                                                                                                                                                               WO200012113-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                          24-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magilavy D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis
                                                                                                                                                                                                                                                                                                                        therapy.
                                                                                                                                                                                                     Y83136;
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agent inhibits CD2 signalling and T cell proliferation and activation and more particularly modulates the number and/or distribution of and more particularly modulates the number and/or distribution of memory effector T lymphocytes. The method can be used for treating a condition in a subject where the condition is characterized by memory effector T lymphocytes playing a role in the pathogenesis of the condition such as psoriatic arthritis, rheumatoid arthritis, multiple solerosis, atopic dermatitis, unclination and where the method comprises administering to the subject lymphoma and where the method comprises administering to the subject an amount of CD2 binding agent sufficient to modulate the memory effector T lymphocytes. The methods provide inhibition of antigen specific interactions for all antigens present, inhibition of T cell

activation, no general immunosuppression, and possibly induction of

347 AA;

tolerance Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming growth factor-beta receptor; TGF-beta receptor; arthritis; fusion protein; fibroproliferative disorder; diabetic nephropathy; glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disorder; therapy; rabbit.
                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kidney, intraocular or pulmonary fibrosis, especially selected from diabetic nephropathy, glomerulonephritis, proliferative vitreoretinopathy, or myelofibrosis. The fusion proteins can also be to treat collagen vascular disorders, including systemic sclerosis, polymyositis, scleroderma, dermatomyositis, and systemic lupus
                                                                                                                          DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                         KGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLD
                                                              1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                                                                                                                                                                                   SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                   Indels
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                              0;
Score 1234; DB 2
Pred. No. 1e-75;
L; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 18-19; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treat fibroproliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
 54.9%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit TGFbetaRII:Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cate R, Gotwals P,
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                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9848024-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctólagus
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                              227;
 Query Match
Best Local S:
Matches 227;
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W73513
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Synthetic.
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Matches 227
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 erythematosus. They can also be administered following coronary angioplasty, to prevent restenosis or scarring and reclosing of arteries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The encoded protein is an example of a protein of the invention, which are isolated TGF-beta receptor fusion proteins that competitively inhibit binding of TGF-beta to TGF-beta receptor. The fusion protein can be used in a method for lowering the levels of TGF-beta in an individual having arthritis. It can also be used to treat medical conditions such as fibroproliferative disorders. The fibroproliferative disorders is kidney, intraocular or pulmonary fibrosis, especially selected from
                                                                                                                                                                                                                                                                                                                                                                                                        Transforming growth factor-beta receptor; TGF-beta receptor; arthritis; fusion protein; fibroproliferative disorder; diabetic nephropathy; glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis; collagen vascular disorder; therapy; human.
                                                                                                                                                                                                           61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                                                               KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a fusion protein of the human transforming growth
                                                                                                                                                               1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                               Length 388;
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                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming growth factor-beta receptor fusion protein treat fibroproliferative disorders
erythematosus. They can also be administered following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanicola-Nadel M;
                                                               DB 19;
                                                              Score 1234; DB 19
Pred. No. 1.2e-75;
                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Human TGFbetaRII:Fc protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koteliansky V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 19-20; 70pp; English.
                                                                                                                                                                                                                                                                                                                    W73514 standard; Protein; 388 AA
                                                              54.98;
99.68;
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                                                                                   Matches 227; Conservative
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                                                                         Similarity
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                               Sequence
                                                               Query Match
                                                                          Best Local
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                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                                                        arteries.
                                                                                                                                                                                                                                                                                                                                                                                                 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
diabetic nephropathy, glomerulonephritis, proliferative vitreoretinopathy, or myelofibrosis. The fusion proteins can also be to treat collagen vascular disorders, including systemic sclerosis, polymyositis, scleroderma, dermatcomyositis, and systemic lupus erythematosus. They can also be administered following coronary angioplasty, to prevent restenosis or scarring and reclosing of arte
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                                                                                                                                                                                                                                                                 Length 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                   Score 1234; DB 19;
Pred. No. 1.2e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y54063 standard; Protein; 388 AA
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                                                                                                                                                                                                                                                                 54.9%;
99.6%;
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                                                                                                                                                                                                                                                                                                                        Conservative
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N-PSDB; Z45251, Z45252.
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Homo sapiens.
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                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09965948-A1
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                                                                                                                                                                                                                                                                                                                        227;
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98US-0089452.

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(BIOJ ) BIOGEN INC.
                                                      16-JUN-1998;
                                                                                 The present sequence represents a splice variant of a rabbit transforming growth factor-beta (TGF-beta) type II receptor fused to the Fc portion of human iggl. The fusion protein has higher affinity for TGF-beta than cusion proteins comprising the non-variant form of the receptor. The fusion protein contains soluble TGF-beta receptor constructs that are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TGF-beta. The protein competitively inhibits binding of TGF-beta to cellular receptors and/or forms an inactive complex with TGF-beta. The protein is used to reduce levels of TGF-beta, for treatment of arthritic conditions associated with overexpression of TGF-beta, especially fibroproliferative diseases, e.g. renal, intra-ocular or pulmonary fibrosis; diabetic nephropathy; myelofibrosis; collagen vascular disease, e.g. systemic lupus erythematosus; and collerant disease, e.g. systemic lupus erythematosus; and collerant overproduction of connective tissue and so prevent adhesions or scarring, and to prevent post-radiation fibrosis (by administration to patients about to undergo radiation therapy).
Disclosure, Page 62-63; 69pp; English.
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DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYRCKVSNKALPAPIEKTISKA 120 Gaps 1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60 . 0 Length 388; Indels DB 21; Pred. No. 1.2e 1; Mismatches Score 1234; 54.9%; 99.6%; Best Local Similarity 99.6 Matches 227; Conservative Similarity Query Match 221 61 ô g g ŏ

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KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180 281 kgqprepqvytlppsrdeltknqvsltclvkgfypsdlavewesngqpennykttppvld 340 121 g ολ

SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228 181 ò g

RESULT 12

Y54064 standard; Protein; 388 Y54064

Y54064;

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27-MAR-2000 (first entry)

Amino acid sequence for TGF-beta type II receptor variant/IgGl fusion. Splice variant; human; transforming growth factor-beta; TGF-beta;

type II receptor; Fc portion; human IgG1; fusion protein; arthritis; fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis; diabetic nephropathy; glomerulonephritis; collagen vascular disease; proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis; polymyositis; scleroderma; dermatomyositis; systemic Lupus erythematosus; restenosis; wound; connective tissue production; adhesion; scarring; post-radiation fibrosis

Homo sapiens Synthetic

W09965948-A1

23-DEC-1999

99WO-US13629. 16-JUN-1999;

angiogenesis; antisclerotic; antiinflammatory; immunosuppressive; can cytostatic; virucide; hepatotropic; antiangiogenic; treatment; fibros; Human; interferon-beta-1a; IFN-beta-1a; immunoglobulin; fusion protei

Human interferon-beta-la/mouse IgG2a Fc fusion protein.

(first entry)

31-JUL-2000

Y70867;

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Y70867 standard; Protein; 399

RESULT 13

£70867

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growth factor-beta (TGF-beta) type II receptor fused to the FC portion of human IgG1. The fusion protein has higher affinity for TGF-beta than fusion proteins comprising the non-variant form of the receptor. The fusion protein comprising the non-variant form of the receptor. The fusion protein contains soluble TGF-beta receptor constructs that are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TGF-beta. The protein competitively inhibits binding of TGF-beta coellular receptors and/or forms an inactive complex with TGF-beta. The protein is used to reduce levels of TGF-beta, for treatment of arthritic conditions associated with overexpression of TGF-beta, especially fibroproliferative diseases, e.g. renal, intra-ocular or pulmonary fibrosis; diabetic nephropathy; collagen vascular disease, e.g. systemic sclerosis, polymyositis, scleroderma, dermatomyositis or systemic lupus erythematosus; and fibrosis associated with reatmons of restenosis. It is also used for treating wounds, to prevent overproduction of connective tissue and so prevent adherenced to the connective tissue and so prevent addition and connective tissue and so prevent and connective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a splice variant of a human transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein of a splice variant of transforming growth receptor, for inhibiting the growth factor, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adhesions or scarring, and to prevent post-radiation fibrosis (administration to patients about to undergo radiation therapy).
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                                                                                                                                          Sanicola-Nadel M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.9%; Score 1234; DB 21;
99.6%; Pred. No. 1.2e-75;
1ve 1; Mismatches 0;
                                                                                                                                          Cate R,
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 64; 69pp; English.
                                                                                                                                          Gotwals P,
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Matches 227; Conservative
                                                                                                                                                                                                                         N-PSDB; Z45253, Z45254.
                                                                                                                                                                                                                                                                                                              factor-beta receptor,
treatment of fibrosis
                                                                                                                                                                                               WPI; 2000-106083/09
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                                                                                                                                                                                                                                                                                 New fusion
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Y70868
ID Y70868 standard; Protein; 418 AA.
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multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; mouse; IgG2a Fc domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon-beta (IRN-beta) especially IRN-beta-13, linker groups and non-IRN-beta proteins, especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein that consists of mature human IRN-beta-1a and mouse IgG2a Fc domain separated by an enterokinase linker. The fusion protein is useful for inhibiting anglogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by
                                                                                                                                                                                                                                                                                                                                                                     Fusion proteins comprising interferon-beta-la useful for inhibiting angiogenesis -
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                                                                                                                                     /label- Mouse_IgG2a_Fc_portion
/note- "comprises the hinge region, CH2 and CH3
constant domains of mouse Ig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
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Pred. No. 1.2e-75;
1; Mismatches 0;
                                                                                          /label= natural_human_IFN-beta-la
                                                                                                                                                                                                                                                                                                               Hochman P;
                                                                                                     167..171
/label= Enterokinase_linker
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                                                                   Location/Qualifiers
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99.6%;
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                                  Homo sapiens.
Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399
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Chimeric
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Protein
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Matches
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Human; interferon-beta-la; IEN-beta-la; immunoglobulin; fusion protein; anglogenesis; antisclerotic; antiinflammatory; immunosuppressive; cancer; cytostatic; virucide; hepatotropic; antianglogenic; treatment; fibrosis; multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; IgG1 Fc domain; VCAM-1; mutant; vascular cell adhesion molecule-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon-beta (IFN-beta) especially IFN-beta-1a, linker groups and non-IFN-beta proteins, especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein consisting of a vascular cell adhesion molecule-1 (VCAM-1) signal sequence, a modified human IFN-beta-1a and human IgG1 Fc domain, which are directly fused without a linker sequence. The fusion protein is useful for inhibiting angiogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type IFN-beta-la Gly at position 162 is substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                             Human interferon-beta-la G162C-IgG1 Fc direct fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                  1..24
/label= VCAM-1_signal_sequence
/note= "Vascular cell adhesion molecule-1"
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/label= natural_human_IFN-beta-la
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Pred. No. 1.3e-75;
1; Mismatches 0;
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99.6%;
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99US-0120237
(first entry)
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Best Local Similarity 99.6
Matches 227; Conservative
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31-JUL-2000
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                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                          Human; interferon-beta-la; IFN-beta-la; immunoglobulin; fusion protein; anglogenesis; antisclerotic; antinflammatory; immunosuppressive; cancer; cytostatic; virucide; hepatotropic; antiangiogenic; treatment; fibrosis; multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; 1961 Fc domain; VCAM-1; mutant; vascular cell adhesion molecule-1; G4S linker.
                   250
                                                 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                               KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type IFN-beta-1a Gly at position 162 is substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising interferon-beta-1a useful for inhibiting
           MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                        Human interferon-beta-la G162C/G4S linker/IgG1 Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197..423
//Label= Human_IgG1_Fc_portion
//note= "comprises hinge, CH2 and CH3 domains of IgG1 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                        1..24
/label- vCAM-1_signal_sequence
/note= "Vascular cell adhesion molecule-1"
                                                                                                                                  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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|abel= natural_human_IFN-beta-1a
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                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/label= G4S_linker
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                                                                                                                                                                                            Y70869 standard; Protein; 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0104491
                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion proteins angiogenesis -
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Synthetic.
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16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                     and
The patent discloses fusion proteins comprising glycosylated interferon-beta (IFN-beta) especially IFN-beta-la, linker groups and non-IFN-beta proteins, especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein consisting of a vascular cell adhesion molecule-I (VCAM-I) signal sequence, a modified human IFN-beta-la which is linked to human IgG1 Fc domain via a G4S linker sequence. The fusion protein is useful for inhibiting anglogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 1234; DB 21;
.larity 99.6%; Pred. No. 1.3e-75;
Conservative 1; Mismatches 0;
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Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                  423 AA;
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